

SEQUENCE LISTING

<100> University of Utah Research Foundation

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AUG 11 1990

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PIPE JOINT
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PATENT & TRADE

100 G-Extrinsically Concoctin Peptides

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<113> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 12 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Trp or bromo-Trp

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CL11 Conus gloriamaris

CL12 SITE

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17 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo
-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

CL14 5
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
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CL17 DNA
CL18 Conus omaria

CL19 CDS
CL20 (146)...(235)

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 ay be Pro or hydroxy-Pro
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1100 13
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 1113 Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue
 9 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp
 or bromo-Trp; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1100 16
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 1 5 10 15

Ser Gly Xaa Asn Cys Ile Ile Phe Phe Cys Leu
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 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu 30
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 ttt ccc aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His 45
 35 40
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 Asn His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu 60
 50 55
 cca ata cag gtc aag cgg tct cgt aaa gaa cat caa ctt tgt gat ctg 240
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu 75
 65 70
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 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu 60
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 <217> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29
 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Glu or gamma-

24. Haa at residue 24 may be Tyr, 125-¹-Tyr, mono-1000-Tyr, or 1000-Tyr, 0-sulpho-Tyr or 0-phospho-Tyr

2: Val Lys Met Cys Arg Lys Met His Gln Leu Cys Asp Leu 15

Met Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile
25 30

12. *Corvus falli*

2) . . (291)

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 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 5 10 15

TTC TTT TTC CTC ACG GGT GAT GAC TGG GGA AAT GGA ATG GAG AAT CTT
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96

144
 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200
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 35 40 45

543 546 549 552 555 558 561 564 567 570 573 576 579 582 585 588 591 594 597 600 603 606 609 612 615 618 621 624 627 630 633 636 639 642 645 648 651 654 657 660 663 666 669 672 675 678 681 684 687 690 693 696 699 702 705 708 711 714 717 720 723 726 729 732 735 738 741 744 747 750 753 756 759 762 765 768 771 774 777 780 783 786 789 792 795 798 801 804 807 810 813 816 819 822 825 828 831 834 837 840 843 846 849 852 855 858 861 864 867 870 873 876 879 882 885 888 891 894 897 900 903 906 909 912 915 918 921 924 927 930 933 936 939 942 945 948 951 954 957 960 963 966 969 972 975 978 981 984 987 990 993 996 999 1002 1005 1008 1011 1014 1017 1020 1023 1026 1029 1032 1035 1038 1041 1044 1047 1050 1053 1056 1059 1062 1065 1068 1071 1074 1077 1080 1083 1086 1089 1092 1095 1098 1101 1104 1107 1110 1113 1116 1119 1122 1125 1128 1131 1134 1137 1140 1143 1146 1149 1152 1155 1158 1161 1164 1167 1170 1173 1176 1179 1182 1185 1188 1191 1194 1197 1200 1203 1206 1209 1212 1215 1218 1221 1224 1227 1230 1233 1236 1239 1242 1245 1248 1251 1254 1257 1260 1263 1266 1269 1272 1275 1278 1281 1284 1287 1290 1293 1296 1299 1302 1305 1308 1311 1314 1317 1320 1323 1326 1329 1332 1335 1338 1341 1344 1347 1350 1353 1356 1359 1362 1365 1368 1371 1374 1377 1380 1383 1386 1389 1392 1395 1398 1401 1404 1407 1410 1413 1416 1419 1422 1425 1428 1431 1434 1437 1440 1443 1446 1449 1452 1455 1458 1461 1464 1467 1470 1473 1476 1479 1482 1485 1488 1491 1494 1497 1500 1503 1506 1509 1512 1515 1518 1521 1524 1527 1530 1533 1536 1539 1542 1545 1548 1551 1554 1557 1560 1563 1566 1569 1572 1575 1578 1581 1584 1587 1590 1593 1596 1599 1602 1605 1608 1611 1614 1617 1620 1623 1626 1629 1632 1635 1638 1641 1644 1647 1650 1653 1656 1659 1662 1665 1668 1671 1674 1677 1680 1683 1686 1689 1692 1695 1698 1701 1704 1707 1710 1713 1716 1719 1722 1725 1728 1731 1734 1737 1740 1743 1746 1749 1752 1755 1758 1761 1764 1767 1770 1773 1776 1779 1782 1785 1788 1791 1794 1797 1800 1803 1806 1809 1812 1815 1818 1821 1824 1827 1830 1833 1836 1839 1842 1845 1848 1851 1854 1857 1860 1863 1866 1869 1872 1875 1878 1881 1884 1887 1890 1893 1896 1899 1902 1905 1908 1911 1914 1917 1920 1923 1926 1929 1932 1935 1938 1941 1944 1947 1950 1953 1956 1959 1962 1965 1968 1971 1974 1977 1980 1983 1986 1989 1992 1995 1998 2001 2004 2007 2010 2013 2016 2019 2022 2025 2028 2031 2034 2037 2040 2043 2046 2049 2052 2055 2058 2061 2064 2067 2070 2073 2076 2079 2082 2085 2088 2091 2094 2097 2100 2103 2106 2109 2112 2115 2118 2121 2124 2127 2130 2133 2136 2139 2142 2145 2148 2151 2154 2157 2160 2163 2166 2169 2172 2175 2178 2181 2184 2187 2190 2193 2196 2199 2202 2205 2208 2211 2214 2217 2220 2223 2226 2229 2232 2235 2238 2241 2244 2247 2250 2253 2256 2259 2262 2265 2268 2271 2274 2277 2280 2283 2286 2289 2292 2295 2298 2301 2304 2307 2310 2313 2316 2319 2322 2325 2328 2331 2334 2337 2340 2343 2346 2349 2352 2355 2358 2361 2364 2367 2370 2373 2376 2379 2382 2385 2388 2391 2394 2397 2400 2403 2406 2409 2412 2415 2418 2421 2424 2427 2430 2433 2436 2439 2442 2445 2448 2451 2454 2457 2460 2463 2466 2469 2472 2475 2478 2481 2484 2487 2490 2493 2496 2499 2502 2505 2508 2511 2514 2517 2520 2523 2526 2529 2532 2535 2538 2541 2544 2547 2550 2553 2556 2559 2562 2565 2568 2571 2574 2577 2580 2583 2586 2589 2592 2595 2598 2601 2604 2607 2610 2613 2616 2619 2622 2625 2628 2631 2634 2637 2640 2643 2646 2649 2652 2655 2658 2661 2664 2667 2670 2673 2676 2679 2682 2685 2688 2691 2694 2697 2700 2703 2706 2709 2712 2715 2718 2721 2724 2727 2730 2733 2736 2739 2742 2745 2748 2751 2754 2757 2760 2763 2766 2769 2772 2775 2778 2781 2784 2787 2790 2793 2796 2799 2802 2805 2808 2811 2814 2817 2820 2823 2826 2829 2832 2835 2838 2841 2844 2847 2850 2853 2856 2859 2862 2865 2868 2871 2874 2877 2880 2883 2886 2889 2892 2895 2898 2901 2904 2907 2910 2913 2916 2919 2922 2925 2928 2931 2934 2937 2940 2943 2946 2949 2952 2955 2958 2961 2964 2967 2970 2973 2976 2979 2982 2985 2988 2991 2994 2997 3000 3003 3006 3009 3012 3015 3018 3021 3024 3027 3030 3033 3036 3039 3042 3045 3048 3051 3054 3057 3060 3063 3066 3069 3072 3075 3078 3081 3084 3087

240
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 Pro Asp Cys Leu Gln Gly Glu Ser Cys Pro
 80 75 70

288
 ... tgc
 ... cat tgc gtt ctt gtc tot tgc
 ... His Cys Val Leu Val Ser Cys
 ... 90 95

nt: tgaactacg gtgatgtatt ctctccatc
/g

12. 1981
13. 1981

Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

Asp His Ser Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
6 70 75 80

Leu Ser Phe Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
35 90 35

10 20

11 201

1. PAT

1. *Corvus dalli*

23-

21- CITE

21 (130)
22 Xaa at residues 3 and 13 may be Phe or hydroxy-Pro; Xaa at residue
23 6 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may
24 be Trp or bromo-Trp

424 · 29

1	Val	Lys	Xaa	Cys	Ser	Xaa	Xaa	Gly	Gln	Leu	Cys	Asp	Xaa	Leu	Ser	Gln
2										10					15	

Asn Cys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val
20 25 30

22.1

406

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Forma textile

2011 QDS

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ttt tto acc ggc tgg aca ttt ggc acg gct gat gac ccc aga aat tga 97
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

145

146 gaa aat ctt ttt tgg aat gca cat cac gaa atg aag aac ccc gaa
147 Ser Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu
35 40

193

aat tta tta gac aac aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241
 Aca Leu Leu Asp Glu Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val 75

tgc aca taaaactgac gtgatgtctt ctcttccctt ctgtctacac tggcttgac 297

Cys Thr

ttagat'gga ggggtggttt cactggttat gaaccccccc cccccccccc cccccccccc 357

tggggcttc tggaggcttc gggggcttaa catcaataa aagt'acag; 406

1110 21
1111 78
1112 P&T
1113 Genus textile

1110 21
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Ile Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asp Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

1110 23
1111 27
1112 P&T
1113 Genus textile

1110 23
1111 SITE
1112 (11...27)
1113 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1110 23
Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

1110 24
1111 27
1112 P&T
1113 Genus textile

1110 24
1111 SITE
1112 (11...26)
1113 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
Glu or gamma-carboxy-Glu; Xaa at residue 9 is Ile; Xaa at residue
20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
yr or O-phospho-Tyr

1110 24
Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Met Cys Ile Val Leu Val Cys Thr
 20 25

421 15
 422 165
 423 DNA
 424 Conus magus

425
 426 PDS
 427 (21) (224)

428 25 48
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 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

429 96
 ttt aag ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

430 144
 ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc ttt aaa ttg
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

431 192
 aag aag aag tgg tgc aaa caa aag ggt gaa atg tgt aat ttg tta gac
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

432 234
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 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

433 265
 caaactggg gtgaigtatt ctctccctctt

434 26
 435 78
 436 PBT
 437 Conus magus

438 26
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

439 30
 tgg thr phe ala thr ala asp asp pro arg asn gly leu gly asn leu
 20 25 30

440 40
 phe ser asn ala his his glu met lys asn pro glu ala ser lys leu
 35 40 45

441 50
 asn lys arg trp cys lys gln ser gly glu met cys asn leu leu asp
 55 60

442 70
 tta asn cys cys asp gly tyr cys ile val leu val cys thr
 75

443 17
 444 17
 445 PBT
 446 Conus magus

447
 448 SITE
 449 (1) (27)

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<118> *Conus distans*

<119> 30

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 1 5 10 15

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 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Glu Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<120> 81

<121> 87

<122> PPT

<123> *Conus distans*

<124> 120

<125> SITE

<126> (1)...(27)

<127> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 1, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<128> 21

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Pro Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

<129> 22

<130> 165

<131> CHA

<132> *Conus ammiralis*

<133> 120

<134> PFS

<135> (1)...(234)

<136> 82

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 1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

taa tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

atc aag agg tgg tgc aaa caa aac ggt gaa atg tgt aat ttg tta gac 192
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

234

taatattgca gttatatttt cttctcccttt c
 265

4110 33
 4111 78
 4112 PPT
 4113 *Conus ammiralis*

4114 33
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Ile Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

His Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Asp Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

His Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

4115 34
 4116 77
 4117 PPT
 4118 *Conus ammiralis*

4119 SITE
 4120 (1)..< (2)
 4121 Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 7 and 1
 4122 s may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr,
 1,5-i-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr

4123 34
 Met Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Lys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

4124 35
 4125 156
 4126 CNA
 4127 *Conus balli*

4128
 4129 PPS
 4130 (1)..< (205)

4131 35
 Met Asn Cys acg tgc gtc atg atc gtt gct gtc ctg ttc ttg acc gcc
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

48

Met Asn Cys acg gct gat gac ccc aga aat gga ttc gag aat ctt
 Met Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

96

ttt atg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat 144
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 45 45
 gaa aag tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca gaa 192
 Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
 55 60
 tgc tgc ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtctt 245
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
 65 70 75
 cct gctgctc c 256
 -1100- 36
 -111- 74
 -112- PPT
 -113- *Conus dalli*
 -1100- 36
 Met Arg Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Tgt Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45
 gln Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
 50 55 60
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
 65 70 75
 -1100- 37
 -111- 25
 -112- PPT
 -113- *Conus dalli*
 -1100- 37
 -111- SITE
 -112- (1)..(25)
 -113- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 15 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 1:5-I-
 Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 -1100- 37
 Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys
 1 5 10 15
 Gly Xaa Cys Ile Leu Leu Phe Cys Thr
 20 25
 -1100- 38
 -111- 441
 -112- LNA
 -113- *Conus gloriamaris*
 -1100- 38
 -111- CTS
 -112- (70)..(300)
 -1100- 38

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 1 5 10
 acc ggc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 153
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
 15 20 25 30
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 Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
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 50 55 60
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 Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
 65 70 75
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 aacacagc acatgacaa a 441
 100 39
 111 77
 112 PRT
 113 *Conus gloriamaris*
 140 39
 Met Lys Ile Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala 15
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 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile 30
 35
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
 40 45
 Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln 60
 50 55 60
 Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro 75
 65 70 75
 100 10
 111 76
 112 PRT
 113 *Conus gloriamaris*
 140 40
 111 SITE
 112 (1)...(26)
 113 Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 26 may be Pro or hydroxy-Pro
 140 40
 Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Asn Cys Cys 15
 1 5 10

Gln Gly Thr Cys Val Phe Phe Cys Leu Xaa
20 25

<210> 41
<211> 446
<212> MVA
<213> *Conus gloriamaris*

<214>
<215> CDS
<216> (74)..(104)

440 41
ggatctctgg accgtgaatt tggcttcaca gttttccact gtggttttc gcatcatcca 60
aactatccc aag atg aaa ctg aag tgc atg atg atc gtt gct gtg ctg 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10
ttt ctt acc gcc tgg aca ttc gcc acg gct gat gat ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25
ttt gag aaa ctt ttt tgg aat aca cat cac gaa atg aag aac ccc gaa 205
Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu
30 35 40
gtt ctt aaa ttg aac atg agg tgc aaa caa gct gat gaa tct tgt aat 253
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn
45 50 55 60
gta ttt cta ctt gac tgc tgc acc gcc tta tgc ttg gga ttc tgc gta 301
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val
65 70 75
ttt tctgtcttc taactccctc tctgtacct gctttgatct ttgattggc 354
Ser
tgtgctttc atgtgttatg aacccccctg atccgattct ttgcggcct cgggggttca 414
aatccccaat aaagcgacag cacaataaaa aa 446
416 42
417 77
418 PFT
419 *Conus gloriamaris*
400 42
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu
20 25 30
Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu
50 55 60
Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
65 70 75

4110- 12
 4111- 16
 4112- EFT
 4113- *Conus gloriamaris*

4114-
 4115- SITE
 4116- (1)..(26)
 4117- Naa at residue 6 may be Glu or gamma-carboxy-Glu.

4118- 43
 4119- Lys Gln Ala Asp Xaa Ser Cys Asn Val Phe Ser Leu Asp Cys Cys
 1 5 10 15

4120- Gly Leu Cys Leu Gly Phe Cys Val Ser
 20 25

4121- 44
 4122- 142
 4123- USA
 4124- *Conus gloriamaris*

4125-
 4126- CDS
 4127- (1)..(225)

4128- 44
 4129- Arg Asn Ctg Acg tgc atg atg atc gtt gct gtc tgc ttc ttg acc acc 48
 4130- Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr 15
 1 5 10

4131- ttc acc acg gcc atc acc agg aat gga ttg ggg aat ctt ttt 96
 4132- Thr Phe Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe 30
 20 25

4133- aat aat cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg aac 144
 4134- Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn 45
 35 40

4135- agt tgc gtt cca tac gag ggc cct tgt aat tgg ctt aca caa aac 192
 4136- Arg Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn 60
 50 55 60

4137- tct gat gag cta tgc gta ttc ttc tgc cta taaaactagc ctgatgt 242
 4138- Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu 75
 65 70

4139- 45
 4140- 75
 4141- EFT
 4142- *Conus gloriamaris*

4143- 45
 4144- Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

4145- Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
 20 25 30

4146- Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45

4147- Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
 50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

110 46
111 48
112 PFT
113 *Conus gloriamaris*

114
115 SITE
116 (1)..(25)
117 Xaa at residue 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue 4 may be Tyr, 1,5-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-ca
rboxy-Glu; Xaa at residue 10 may be Trp or bromo-Trp

118 16
Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu
20 25

119 47
120 50
121 DNA
122 *Conus magus*

123
124 CPS
125 (1)..(231)

126 47
atg aag ctg acg tgg gtt atg atc gtt ggt gtt etc ttc ttg acc gtc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val 15
1 5 10

127 aag aac ttc gcc acg ggt gat gac tcc gga aat gga ttg gag aag ctt 96
Trp Phe Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu 50
1 20 25

128 ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aag ttg 144
Thr Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
1 25 40

129 aag aag tgg tgc aag caa ggt gat gaa cct tgt gat gta ttt tca ctt 192
Asp Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu 55 60
1 50

130 tgg tgc acc gcc ata tgt ctt gga ttc tgc acg tgg tgaatgtcttc 241
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp 70 75
1 65

131 250

132 48
133 57
134 PFT
135 *Conus magus*

136 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Cys Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Ile Pro Cys Asp Val Phe Ser Leu
50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

116- 49

111- 16

112- RPT

113- *Conus magus*

120-

121- SITE

122- (1)...(26)

123- Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residue 26 may be Trp or bromo-Trp

140- 40

Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
20 25

110- 60

111- 1-4

112- CIA

113- *Conus textile*

120-

121- CDS

122- (1)...(295)

100- 50
acattgcaag ggaatttgg attcatagtt ttcaactgtc gtctttggca tcatccaaaa 60

caacacaaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttt acc gac tgg aca ttc gcc acg gct tat gac tcc agc aat gga ttg 157
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu
15 20 25

aga aat ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct 205
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser
30 35 40 45

aaa ttg aac cag acg tgc ctt gat gct ggt gaa gtt tat gat att ttt 253
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe
50 55 60

ttt cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca 295
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

taaaattacc gtgatgtctt ctactccct ctgtgtctacc tggcttgatc ttgtattggc 355

gattacatt tactgttat gaaacccctg atccagttct ctggaggcct cgggggttca 415

appttcaat aaagcgaca 434

417 51
418 75
419 PPT
420 Conus textile

442 51
Met Tyr Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
20 25 30

Phe Leu Tyr Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Gln Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

417 51
418 75
419 PPT
420 Conus textile

417 51
418 75
419 PPT
420 Conus textile

442 51
Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys
1 5 10 15

443 51
Gly Xaa Cys Ile Leu Leu Phe Cys Ala
1 5 10 15

417 51
418 75
419 PPT
420 Conus textile

417 51
418 75
419 PPT
420 Conus textile

442 51
Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys
1 5 10 15

443 51
Gly Gly Val Cys Phe Leu Met Ala Cys Ile
1 5 10 15

417 51
418 75

4011 PPT
4012 Conus textile

4020

4021 SITE

4022 (1)... (24)

4023 Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

4040 54

Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Xaa Asn Cys Cys
1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu
20 25

4100 55

4101 560

4102 D6P

4120 Conus emaria

4140

4141 GDS

4142 (1)... (140)

4143 59
atg ana cgg aag tgc atg atg atc gtt gct gtg ctg ttc tgg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc acc aag gct gat gac ccc aga aat gga ttg gag aat ttt 36
Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

taa taa aag aca aca cac gaa atg aag aac ccc gaa gcc tat aaa ttg 144
Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

atc aag aag tac cta gca gaa cat gaa act tat aat ata ttt aca caa 192
Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
50 55 60

atc tac tgc aca gcc gtg tgc att ttt atc tgc gta caa gct cca gag 240
Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
65 70 75 80

atatgtatttactcccccctc 260

4160 56

4161 80

4162 PPT

4180 Conus emaria

4190 56

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
60 55 60

Asn Lys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
65 70 75 80

110- 5'
111- 19
112- PPT
113- *Onchus emaria*

114-
115- SITE
116- (1)...(29)
117- Xaa at residues 4, 6, 17 and 29 may be Glu or gamma-carboxy-Glu;
Xaa at residue 28 may be Pro or hydroxy-Pro

118- 17
119- Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys
1 5 10 15

Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa
20 25

119- 18
120- 261
121- PMA
122- *Onchus emaria*

123-
124- CDS
125- (1)...(261)

126- 58
127- aaa ctg act gtc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
128- Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

129- tta aat ttt acc acg gct gaa gac ccc aga cat gga ttg gag aat ctt 96
130- Thr Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
10 25 30

131- ttt ctg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
132- Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

133- gat aag agt tgc att cca cat ttt gac cct tgt gat cag ata cgc cac 192
134- Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
50 55 60

135- aat tat tgc ttt ggc ctg tgc cta cta ata gcc tgc atc taaaactgcc 241
136- Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
65 70 75

137- gaaatattt gttccacatc 261

138- 54
139- 70
140- PPT
141- *Onchus emaria*

142- 50
143- Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
 10 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
 35 40 45

Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
 50 55 60

Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 65 70 75

110 80

111 85

112 90

113 95

114 100

115 105

116 110

117 115

118 120

119 125

120 130

121 135

122 140

123 145

124 150

125 155

126 160

127 165

128 170

129 175

130 180

131 185

132 190

133 195

134 200

135 205

136 210

137 215

138 220

4.12. Cenus omaria

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Ser Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
20 25 30

Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
45 40 45

Asp Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
55 60

Asp Cys His Gly Tyr Cys Val Gly Ala Ile Cys Leu
62 70 75

10-63

— 11 —

$$- \frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx + \frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla v|^2 dx$$

1948 *Corvus omaria*

192

SIZE

(25)

14-15- Xaa at residue 16 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
 Cys Leu Gly Phe Gly Xaa Ala Cys Leu Ile Leu Xaa Ser Asp Cys Cys
 5 10 15

Gly Asn Cys Val Gly Ala Ile Cys Leu
26 25

1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

6.2

2.11A

Genus aulicus

2000

1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 26

12) . . (240)

100 64
 441 aag atg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 442 Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 10 15

TTT ACC TTC GGC ACG GCT GAT GAC TCC AGA AAT GGA TTG GAG AAT CTT
 Phe Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 25 30

144
 ... tta aag aca caa cac aaa atg aag aac ccc gaa gcc tct aaa ttg
 ... S-1 Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
 3 45

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aa: ttt tgc gac ggg aag tgc ctt ctt atc tgc ata caa aat cca cag 240

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

tgatgttttctctctacccttc

262

4010 65
4111 80
4112 PPT
4113 Conus aulicus

4010 61
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

4110 61
4111 80
4112 PPT
4113 Conus aulicus

4110 61
4111 SITE
4112 (1)...(29)
4113 Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 28 may be Pro or hydroxy-Pro

4010 66
Lys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys
1 5 10 15

Arg Gly Thr Lys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
20 25

4110 67
4111 858
4112 RNA
4113 Conus aulicus

4110 67
4111 SDS
4112 (1)...(2-8)

4010 67
Arg aas ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc
1 5 10 15
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala

48

4010 67
Arg aas ttt acc acg gct gat gac ccc aga aat gga ttg gat aat cgt
1 5 10 15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg

96

4010 67
Arg aas ttt acc acg gct gat gac ccc aga aat gga ttg gat aat cgt
1 5 10 15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg

144

25 10 45
 aac aag aag tgc ctt gag ttt ggt gaa ctt tgt aat ttt ttt ttc cca 192
 Aaa Aaa Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Pro
 55 60
 aac aag aag ggc tat tgc gtt ctt ctt gtc tgc cta taaactaacg 238
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75
 caagagcttttcttctccctc 258
 110 68
 111 74
 112 PPT
 113 *Conus aulicus*
 120 68
 Aaa Cys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Thr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
 20 25 30
 Phe Aaa Cys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
 35 40 45
 Aaa Cys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
 50 55 60
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75
 110 68
 111 74
 112 PPT
 113 *Conus aulicus*
 120 68
 121 SITE
 122 (1)..(25)
 123 Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 121-1-Tyr, mono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr
 130 68
 Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15
 Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25
 110 70
 111 103
 112 LCA
 113 *Conus nalli*
 120 70
 121 103
 122 (1)..(231)
 130 70
 aag aag aag aag tgc gtc atg atc gtt gct gtc ctg ttc ttg acc gcc 48

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 ttg aat ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg 96
 Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu 20 25 30
 ttt tag atg gga cat cac gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 35 40 45
 aat aag aag tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca 192
 Asn Lys Ala Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser 50 55 60
 caa tgc ttc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaactgcc 241
 Asn Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu 65 70 75
 gtatgtcttt ctatatcccc tc 263
 1100 71
 111 77
 112 PFT
 113 Conus dalli
 1100 71
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Phe Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser
 50 55 60
 Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu
 65 70 75
 1100 73
 111 76
 112 PFT
 113 Conus dalli
 1100
 111 PITE
 112 (1) (26)
 113 Gaa at residue 6 may be Glu or gamma-carboxy-Glu.
 1100 71
 Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys
 1 5 10 15
 Phe Gly Val Cys Met Val Phe Phe Cys Leu
 20 25
 1100 73
 111 76
 112 PIA
 113 Conus distans

4210-

4211- CDS
4212 (1)..(222)

4400- 75
atg gaa cta acg tgc gta atg acc gtt gct gta cta ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tta ata ttc gta acc gct gaa gac ccc aga gat gga ttg agg aat ctt 36
Tyr Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
20 25 30
tta tta aat gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
aac gaa agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60
gac tgc tgc acc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238
Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
65 70 75
aaatattctt ctattcccat c 259

4110- 74
4111- 76
4112- PFT
4113- Conus distans

4400- 74
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tta tta tta val thr ala glu arg pro arg asp gly leu arg asn leu
20 25 30
leu ser asn ala arg his glu met lys asn pro glu ala ser lys leu
35 40 45
asn glu arg cys leu gly phe gly glu ala cys leu met leu tyr ser
50 55 60
asp cys cys ser tyr cys val gly ala val cys leu
65 70 75

4110- 75
4111- 85
4112- PFT
4113- Conus distans

4400- 75
4401- SITE
4402- (1)..(25)
4403- Ala at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues
12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
ulpho-Tyr or O-phospho-Tyr

4400- 75
Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
1 5 10 15

Ser Met Cys Val Gly Ala Val Cys Leu
20 25

210- 76
211- 762
212- PNA
213- Conus pennaceus

210- 76
211- 763
212- (1)..< (231)

210- 76 49
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 76 96
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 76 144
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 76 192
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 76 241
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 76 262
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 77
211- 77
212- PFT
213- Conus pennaceus

210- 77
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 77
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 77
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 77
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 77
Met Met Cys Val Gly Ala Val Cys Leu Phe Leu Thr Ala
1 5 10 15

210- 78
211- 78
212- PFT
213- Conus pennaceus

210- 78
211- 78
212- PFT
213- Conus pennaceus

210- 78
211- 78
212- PFT
213- Conus pennaceus

4.3. Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro

4.10 78
Cys Val Lys Xaa Leu Asp Xaa Cys Asp Met Leu Arg His Thr Cys Cys
1 5 10 15

Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
20 25

4.11 79
4.12 259
4.13 CNA
4.14 Conus pennaceus

4.15 CUG
4.16 (11... (228)

4.17 78
Arg AAA CTG AC; TGT GTG ATG ATC GTT GCT GTT CTG TTC TTG ACC GCC 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

4.18 46
TGA AAG TTT GCC ACG GCT GAT GAC ACC AGA AAT GGA TTG GGG AAT CTT
Tyr Met Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
1 5 10 15 20 25 30

4.19 114
TAT TGG GAT GGA CAT CAC GAA ATG AAG AAC CCC GAA GCT TCT AAA TTG
Met Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
1 5 10 15 20 25 30 35 40 45

4.20 192
AAG GAG AGG TGC CTT GGG TTT GGT GAA GTT TGC AAT TTC TTT TTT CCA
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
1 5 10 15 20 25 30 35 40 45 50 55 60

4.21 238
GAT TGC TAC AAC TAT TGC GTT GCT CTT GTC TGC CTA TAAACTACC
Met Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75

4.22 59
GATGTGCTT CTATTCCTT C

4.23 80
4.24 76
4.25 PFT
4.26 Conus pennaceus

4.27 80
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Tyr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
1 5 10 15 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
1 5 10 15 20 25 30 35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
1 5 10 15 20 25 30 35 40 45 50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75

35 40 45
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
 25 55 60
 Thr Lys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 65 70 75 80
 110- 84
 111- 89
 112- TET
 113- *Conus pennaceus*
 120-
 121- TIDE
 122- (11...124)
 123- Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.
 130- 81
 Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys
 1 5 10 15
 Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 20 25
 140- 85
 141- 160
 142- GNA
 143- *Conus pennaceus*
 150-
 151- TFS
 152- (11...140)
 160- 85
 Met Asn Cys Arg Cys tgc ttc atg atc gtt gct gta ctg ttc ttg acc gcc 48
 1 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15
 170- 86
 Met Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe 36
 10 25 30
 180- 87
 Met Thr Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 144
 35 40 45
 190- 88
 Asn Arg Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln 192
 50 55 60
 200- 89
 Met Thr Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu 240
 65 70 75 80
 210- 90
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala 260
 10- 86
 11- 80
 12- TET
 13- *Conus pennaceus*
 140- 86
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30
 Phe Lys Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
 50 55 60
 Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
 65 70 75 80
 110 97
 111 19
 112 187
 113 Conus pennaceus
 114
 115 SITE
 116 (111..129)
 117 Xaa at residues 4, 6 and 19 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 28 may be Pro or hydroxy-Pro
 118
 119
 120 Lys Lys Ala Xaa Ser Xaa Ala Cys Asn Ile Ile Thr Gln Asn Cys Cys
 1 5 10 15
 Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Xaa Xaa
 20 25
 121 63
 122 632
 123 TMA
 124 Conus omaria
 125
 126
 127 CDS
 128 (110)..(199)
 129
 130 63
 131 atgacatc atcatcatca tcatcatc tctcatc tcatcatt catcgtgc 60
 132 caaatgtca taatatattg agtctctctt tctgtttgtg tctgacaga ttg aac aag 118
 133 Leu Asn Lys
 1 1
 134 ttc att gac ggt ggt gaa att tgt gat att ttt ttt cca aac tgc 166
 135 Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe Pro Asn Cys
 5 10 15
 136 agt agt tgg tgc att att ctg gtc tgc gca tgaactacc gtgatgtctt 219
 137 Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
 10 25 30
 138 atctctct ctatgtatg taggcggcgc ctctagaggg tccaagctta cgtatgcgtg 279
 139 atggatgct catagctctt ctatgtgtgc acctaaatcc aattcactgg ccgtgttttt 339
 140 ataacatgct gactgggaaa acctgggct tabcnaactt aatgccttg cagcacatcc 399
 141 caatttgcgc agctgggcta atagggaaga ggacgcacac gatgcgcctt ccaacagttt 459

ggcacatccg aatggggaat gggacgcgcc ctgttagcgcc gcattaagcg cggcggggtgt 519
 ggggggaa cgcagcgtga caggtacact tgcacgcgcc ctacgcgcgc ctccttttgc 579
 ttttttcc tctttttctg ccaccgttag cggggggttt tcccgtaag etc 632
 110- 64
 111- 30
 112- PPT
 113- Conus omaria
 114- 89
 Leu Asn Cys Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe 15
 1 5 10
 Pro Asn Cys Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala 30
 2 20 25
 110- 60
 111- 30
 112- PPT
 113- Conus omaria
 114- 89
 115- SITE
 116- 11... (26)
 117- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 12 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mi-Trp
 118- 89
 Cys Ile Asp Gly Gly Xaa Ile Cys Asp Ile Phe Phe Xaa Asn Cys Cys 15
 1 5 10
 Ser Gly Xaa Cys Ile Ile Leu Val Cys Ala 25
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 112- DNA
 113- Conus omaria
 114- 89
 115- TDS
 116- 107... (196)
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 gggagatc atccatcatg atccatctgt ccacatccac attcattcat tgcgtgcag 60
 ggggtgaaa atattcgagt cctcctctct gtttgtatct gacaga ttg aac aag 115
 1 Leu Asn Lys
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 gga tgc att gac ggt ggt aaa att tgt ggt att ttg ttt cca agc tgc
 Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys 15
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110 92
 111 94
 112 IPT
 113 Conus omaria

110 90
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 1 5 10 15
 111 Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

112 96
 113 98
 114 IPT
 115 Conus omaria

116 90
 117 WIFE
 118 (1)...(26)
 119 Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 120 18 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 121 de-Trp

122 90
 Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
 1 5 10 15
 123 Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
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124 94
 125 WIP
 126 WNA
 127 Conus marmoreus

128 90
 129 CDS
 130 (107)...(193)

131 94
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 132 tgc tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163
 Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys
 5 10 15
 133 tgc gtc tat tgc gtt att ctt gtc tgc cta taaaactacc gtgatgtctt 213

Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
2 25

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118 98
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 121 Genus narmoreus

1460 96
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100 Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile
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 101 5
 102 PRT
 103 Coccus marmoreus

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SITE
(1)..(25)
Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 18 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr,
18-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Tyr

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4060 34
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117: Met Cys Val Leu Leu Leu Cys Ile
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210	100
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213	Conus omnia

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 121 (1) (26)
 131 Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.
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 221 CNA
 231 Cetus omaria

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 402 PPT
 403 *Conus maria*
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 402 PPT
 403 *Conus maria*
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 401 SITE
 402 (11)-(15)
 403 Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr
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454- 197
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 463- Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
 s 23 and 32 may be Pro or hydroxy-Pro

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 113 Conus ammiralis

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 123 Conus ammiralis

124
 125 SITE
 126 (1) (26)
 127 Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro

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 e 19 may be Tyr, 1,25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-
 Tyr or O-phospho-Tyr

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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
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Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25
ttt gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205
Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys
30 35 40
tct tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253
Arg Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp
15 50 55 60
gtt ttt aat tca aaa tgc tgc agt ggt tgg tgc att att atc ttc tgc 301
Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys
65 70 75
gga taaactaac gtgatgttct cactacccct ctgtgctacc tgggttgatc 354
Ala
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35 40 45
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Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala
6 70 75

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4018. *Conus marmoreus*

4000- 119
Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
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Thr Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
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Pro Met Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro
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Ser Lys Cys Ser Gly Trp Cys Ile Val Leu Val Lys Ala
65 70 75

4010- 159

4011- 20

4012- PFT

4013- *Conus marmoreus*

4014-

4015- SITE

4016- 410... 261

4017- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
18 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or pro-
line-Thr

4018- 110

Thr Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
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4019- 121

4020- 470

4021- PNA

4022- *Conus marmoreus*

4023-

4024- PFS

4025- (70)...(303)

4026- 121
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Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu
1 5 10

acc ggc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 159
Thr Ala Thr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
1 20 25 30

att ctt ttt tgg aag gaa cat cac gaa atg aag aac ccc gaa gcc tct 207
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
1 35 40 45

aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt 255
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
1 50 55 60

gaa gaa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303
 Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
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tactatagct tatgtctctt actccctctt gtgtgctgt gcttgatctt tgattggcgc 363

gtgagcttca atggttatga acccccttga tccgactctc ttgcggcttc aggggttcaa 423

Catalsatla agagagacag aaaaatgaaa aaaaaaaaaa aaaaaaa 470

1100 111

1111 78

1112 287

1113 *Onchus marmoreus*

1100 111

Met Tyr Lys Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala 15
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Tyr Trp Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu 30
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Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
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Asn Lys Ala Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln 60
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Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile 75
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1100 111

1111 78

1112 287

1113 *Onchus marmoreus*

1100 111

1111 SITE

1112 1111274

1113 Xaa at residues 2 and 16 may be Pro or hydroxy-Pro; Xaa at residu
 es 6 and 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 a
 nd 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho
 -Tyr or O-phospho-Tyr

1100 111

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys 15
 1 5 10 15

Met Trp Xaa Cys Phe Ile Val Val Cys Xaa Ile 25
 20 25

1100 114

1111 470

1112 104

1113 *Onchus marmoreus*

1100 114

1111 GLS

1112 (67)...(312)

1100 114

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gtttag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
 1 5 10

acc atc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156
 Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu
 15 20 25 30

gag att ctt tat atg aag gca att cac gaa acg gaa aac cac gaa gcc 204
 Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala
 35 40 45

tct aaa ttt aac gtg aga gac gac gag tcc gaa cct cct gga gat ttt 252
 Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe
 50 55 60

tat gac ttc ttt aaa att gga ccc cct tgc tgc agt ggc tgg tgc ttc 300
 Cys Gly Phe Phe Lys Ile Gly Pro Cys Cys Ser Gly Trp Cys Phe
 65 70 75

cct tgg tgc gcc taaaactgcc atgattgttt ctattccct atgtgtacc 352
 Leu Trp Cys Ala
 80

tgtatgatac attgatggcc gctgacctt caatggatat gaacccacct gatccgactc 412
 tcttgggccc tgggggggttc aacatccaaa taagctccac aacacatataa aaaaaaaa 470

110 115
 111 80
 112 PEST
 113 *Conus marmoreus*

140 145
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60

Ile Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

Cys Ala

116 126
 117 80
 118 PEST
 119 *Conus marmoreus*

120
 121 SITE
 122 1) (30)
 123 Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
 s 24 and 28 may be Trp or bromo-Trp

140 145
 Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile

211 19
211 19
211 19T

Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
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Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
61 70 75 80

Cys Ala

<11> 100

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<13> PBT

<14> *Conus omaria*

<15>

<16> SITE

<17> (1...30)

<18> Ala at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
6, 7, 10 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
be Trp or bromo-Tyr

<19> 102

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<21> 103

<22> 107

<23> LNA

<24> *Conus aulicus*

<25>

<26> GPS

<27> (1)...(246)

<28> 108
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Gly Lys Leu Thr Cys Leu Met Ile Val Ala Val Ile Phe Leu Thr Ala
1 5 10 15

ttr aac ttc gtr acg gct gtc cct cac tcc agc aat gca ttc gag aat 36
Tyr Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
1 5 10 15 20 25 30

cca tat ctg tag gca cct ctc gaa atg gaa aac cct gaa gcc tct aaa 144
Arg Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
1 5 10 15 20 25 30 35 40 45

...aa' agc aga jac tac gat tgc gaa cct cct gga aat ttt tct ggc 192
...Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
1 5 10 15 20 25 30 35 40 45 50 55 60

...aa' aaa att ggt cag cct tgc tgc agt gcc tgc tgc ttt ttc gcc 240
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
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...aa' ggt taaactccc gtgatgttt ctcctccct c 177
Met Ala

<29> 104

<30> 105

<31> PBT

<32> *Conus aulicus*

44008 124
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Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

Cys Ala

130 135

136 36

137 PFF

138 Conus nallidus

139

140 SITE

141 1...20

142 Xaa at residue 2 may be Tyr, 135-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

44009 145

Asp Val Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

130 136

131 36

132 INA

133 Conus marmoreus

134

135 FDS

136 (111)...(112)

44010 136
gggagacm atcatcatca tggatccacg tctgacacga tctattcatt cttatgtggc 60

caagctgaaa taatgatgc aagtcctct tctgtgtgt atctgacaga tgg aac 116
Leu Asn
1

acc aga aac jac gat tgc gaa cct cct gga aat ttt tgt agc atg ata 164
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
1 15

aac att agc acc cct tgc tgc aat ggc tgc tct ttt ttc gcc tgc gcc 212
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
20 25 30

taaaatgcc gtgatgtctt ctcttccct ctagtagtag tagggcgagc ctttagagga 272

tccaaagctta cgtacgggtg catgagacgt catagctctt ctatagtgtc acctaaatcc 332
 atttcaactg acctgctttt acaacgttgt gactggggaaa acctatgctt taccacaactt 392
 aatcgctttt cagcacaacc ccttttggtc aactggggtt atagcgaaga ggccggcaac 452
 gctgctctt ccaacaactt ggcagcgtg aatggcgaat gggacggcgc ctgttagcgc 512
 gcttttggcg cggcggtgtt ggtggttaag cggcggcgtt gaccgctac acttgccagg 572
 gcttggcg cggctccttt cgtttttttt cttctttttt cggcagtttc gcggcttttt 632
 cgtggaac totaaatgg gggctctttt agggcgcgat ttaagtcttt tac 685

<117> 147

<211> 34

<112> PBT

<111> *Cynus marmoreus*

<110> 139

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 2 25

Cys Ala

<110> 139

<111> 34

<112> PBT

<110> *Cynus marmoreus*

<111> 139

<112> PBT

<110> 139
 Met at residue 8 may be Glu or gamma-carboxy-Glu; Xaa at residues
 6, 7, 10 and 12 may be Pro or hydroxy-Pro; Xaa at residue 24 may
 be Trp or orono-Trp

<109> 139

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile 15
 1 10

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala 30
 2 25

<110> 139

<111> 34

<112> PBT

<110> *Cynus regius*

<111> 139

<112> PBT

<110> (111-139)

<111> 139

Thr Asp Asp Arg gac tgc ctt agt aaa aac gct ttc tgt gcc cgg ccg 48
 Met Asn Glu Asn Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro 15
 1 10

Arg Thr Gga Ala ctc tgc tgc agt ggt tgg tgc tta tac gtc tgc atg 96
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met 30
 2 25

taaaactgac gtgatgtctt ctatccctc

<11> 11)
<11> 12)
<11> PPT
<11> *Onus regius*

<120> 11)
Leu Asn Glu Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
1 5 10 15

1.6 Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
20 25 30

<12> 111
<12> 12)
<12> PPT
<12> *Onus regius*

<13> 111
<13> 11...108)
<13> Xaa at residues 11 and 12 may be Trp or bromo-Trp; Xaa at residue
13 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be T
yr, 118-1-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
pho-Tyr

<4> 141
Asp Lys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
5 10 15

Leu Lys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met
20 25

<14> 143
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<14> *Onus radiatus*

<15> 143
<15> (11...103)

<16> 141
a tgg aac aac aac ggt gat gac tgc ctt gct gtt aac aac aat tct ggc 49
Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
5 10 15

tct cca aac att gga ggg cca tgc tgc agt ggc ttg tgc ttt ttg gtc 97
Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
20 25 30

<17> gct taaaactgac gtgatgtctt ctatccctc 133
Cys Ala

<18> 143
<18> 14)
<18> PPT
<18> *Onus radiatus*

<19> 143
Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
1 5 10 15

Phe Ser Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
20 25 30

$$C_{\text{eff}} = 1.04$$
[illegible]

001 SITE
 002 10-1-1964
 003 Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.
 004

14 148
 Gly Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu
 5 10 15

(194-11) Ala Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala
25 30

[illegible]
$$j = 1, \dots, (96) \quad (52)$$

1100 1400 48
 tgg atc cag agc gac tgc ctt cct aga gac aca ttc tgt gcc ttg cgg
 Thr Asn Glu Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
 1 5 10 15

96
 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
 GAG GAT GGA GAA GTG TGC TGC AGT GGC GGG TGC TTA CTC TTC TGC GTG
 Glu Asp Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 25 30

127

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146
Asn Glu Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
5 10 15

100 Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
20 25 30

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10 SITE
11 -1)-(28)
12 Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.

<400> 147
 Asn Cys Leu Xaa Arg Asp Thr Phe Cys Ala Leu Xaa Gln Leu Gly Leu
 1 5 10 15

Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 20 25

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 <11> 18A
 <11> *Genus aurisiacus*

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 <211> 103
 <212> 211..(234)

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 1 5 10 15

tta aca ttc gtc ari gct tat gac tcc aga aat gga ctg aag aat ctt 96
 Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

tac aca aag aca cys cat gaa atg aag aac tcc gaa gcc tct aaa ttg 144
 Glu Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

acc aag aca gat gag ttc tct aat gct ggt gca ttt tct ggc atc cat 192
 Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

aaa gga ttc ttc tgc aac gag att tcc att gtt tgg ttc aca 234
 Phe Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
 65 70 75

caaaagcat tctgct gcta catcttgctg cttaaacgga ggact tgcct gcagcaacct 284
 cgtttattt ctgctgctgct thaatatttc gtgatgtcct ctattcccat c 345

<210> 149
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 <11> 18T
 <11> *Genus aurisiacus*

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Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Lys Gly Ile His
 50 55 60

Ile Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
 65 70 75

<210> 150
 <211> 27

213. PPT
214. *Pinus auristatus*

DATE
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4211- 19..(27)
4212- Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may
4213- be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or br
4214- m-Trp

Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
20 25

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1993 213
1994 142

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 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

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25 30

111 113 123 133 143 153 163 173 183 193 203 213 223 233 243 253 263 273 283 293 303 313 323 333 343 353 363 373 383 393 403 413 423 433 443 453 463 473 483 493 503 513 523 533 543 553 563 573 583 593 603 613 623 633 643 653 663 673 683 693 703 713 723 733 743 753 763 773 783 793 803 813 823 833 843 853 863 873 883 893 903 913 923 933 943 953 963 973 983 993 1003 1013 1023 1033 1043 1053 1063 1073 1083 1093 1103 1113 1123 1133 1143 1153 1163 1173 1183 1193 1203 1213 1223 1233 1243 1253 1263 1273 1283 1293 1303 1313 1323 1333 1343 1353 1363 1373 1383 1393 1403 1413 1423 1433 1443 1453 1463 1473 1483 1493 1503 1513 1523 1533 1543 1553 1563 1573 1583 1593 1603 1613 1623 1633 1643 1653 1663 1673 1683 1693 1703 1713 1723 1733 1743 1753 1763 1773 1783 1793 1803 1813 1823 1833 1843 1853 1863 1873 1883 1893 1903 1913 1923 1933 1943 1953 1963 1973 1983 1993 2003 2013 2023 2033 2043 2053 2063 2073 2083 2093 2103 2113 2123 2133 2143 2153 2163 2173 2183 2193 2203 2213 2223 2233 2243 2253 2263 2273 2283 2293 2303 2313 2323 2333 2343 2353 2363 2373 2383 2393 2403 2413 2423 2433 2443 2453 2463 2473 2483 2493 2503 2513 2523 2533 2543 2553 2563 2573 2583 2593 2603 2613 2623 2633 2643 2653 2663 2673 2683 2693 2703 2713 2723 2733 2743 2753 2763 2773 2783 2793 2803 2813 2823 2833 2843 2853 2863 2873 2883 2893 2903 2913 2923 2933 2943 2953 2963 2973 2983 2993 3003 3013 3023 3033 3043 3053 3063 3073 3083 3093 3103 3113 3123 3133 3143 3153 3163 3173 3183 3193 3203 3213 3223 3233 3243 3253 3263 3273 3283 3293 3303 3313 3323 3333 3343 3353 3363 3373 3383 3393 3403 3413 3423 3433 3443 3453 3463 3473 3483 3493 3503 3513 3523 3533 3543 3553 3563 3573 3583 3593 3603 3613 3623 3633 3643 3653 3663 3673 3683 3693 3703 3713 3723 3733 3743 3753 3763 3773 3783 3793 3803 3813 3823 3833 3843 3853 3863 3873 3883 3893 3903 3913 3923 3933 3943 3953 3963 3973 3983 3993 4003 4013 4023 4033 4043 4053 4063 4073 4083 4093 4103 4113 4123 4133 4143 4153 4163 4173 4183 4193 4203 4213 4223 4233 4243 4253 4263 4273 4283 4293 4303 4313 4323 4333 4343 4353 4363 4373 4383 4393 4403 4413 4423 4433 4443 4453 4463 4473 4483 4493 4503 4513 4523 4533 4543 4553 4563 4573 4583 4593 4603 4613 4623 4633 4643 4653 4663 4673 4683 4693 4703 4713 4723 4733 4743 4753 4763 4773 4783 4793 4803 4813 4823 4833 4843 4853 4863 4873 4883 4893 4903 4913 4923 4933 4943 4953 4963 4973 4983 4993 5003 5013 5023 5033 5043 5053 5063 5073 5083 5093 5103 5113 5123 5133 5143 5153 5163 5173 5183 5193 5203 5213 5223 5233 5243 5253 5263 5273 5283 5293 5303 5313 5323 5333 5343 5353 5363 5373 5383 5393 5403 5413 5423 5433 5443 5453 5463 5473 5483 5493 5503 5513 5523 5533 5543 5553 5563 5573 5583 5593 5603 5613 5623 5633 5643 5653 5663 5673 5683 5693 5703 5713 5723 5733 5743 5753 5763 5773 5783 5793 5803 5813 5823 5833 5843 5853 5863 5873 5883 5893 5903 5913 5923 5933 5943 5953 5963 5973 5983 5993 6003 6013 6023 6033 6043 6053 6063 6073 6083 6093 6103 6113 6123 6133 6143 6153 6163 6173 6183 6193 6203 6213 6223 6233 6243 6253 6263 6273 6283 6293 6303 6313 6323 6333 6343 6353 6363 6373 6383 6393 6403 6413 6423 6433 6443 6453 6463 6473 6483 6493 6503 6513 6523 6533 6543 6553 6563 6573 6583 6593 6603 6613 6623 6633 6643 6653 6663 6673 6683 6693 6703 6713 6723 6733 6743 6753 6763 6773 6783 6793 6803 6813 6823 6833 6843 6853 6863 6873 6883 6893 6903 6913 6923 6933 6943 6953 6963 6973 6983 6993 7003 7013 7023 7033 7043 7053 7063 7073 7083 7093 7103 7113 7123 7133 7143 7153 7163 7173 7183 7193 7203 7213 7223 7233 7243 7253 7263 7273 7283 7293 7303 7313 7323 7333 7343 7353 7363 7373 7383 7393 7403 7413 7423 7433 7443 7453 7463 7473 7483 7493 7503 7513 7523 7533 7543 7553 7563 7573 7583 7593 7603 7613 7623 7633 7643 7653 7663 7673 7683 7693 7703 7713 7723 7733 7743 7753 7763 7773 7783 7793 7803 7813 7823 7833 7843 7853 7863 7873 7883 7893 7903 7913 7923 7933 7943 7953 7963 7973 7983 7993 8003 8013 8023 8033 8043 8053 8063 8073 8083 8093 8103 8113 8123 8133 8143 8153 8163 8173 8183 8193 8203 8213 8223 8233 8243 8253 8263 8273 8283 8293 8303 8313 8323 8333 8343 8353 8363 8373 8383 8393 8403 8413 8423 8433 8443 8453 8

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gag ggc gga tgc tcc agt gag tat tgt ctc ccg gcc gtc tgc ttc ggt
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240

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11	PI-T
12	Genus purpurascens

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Tyr Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Tyr Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
5 55 60

Glu Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
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Gly

110 153

111 20

112 PFI

113 *Conus purpurascens*

114

115 SITE

116 111.1(29)

117 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

118 153

211 Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
5 10 15

Cys Lys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

119 153

120 20

121 PFI

122 *Conus purpurascens*

123

124 SITE

125 111.1(29)

126 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

127 153

211 Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
5 10 15

Cys Lys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

128 153

129 20

130 PFI

131 *Conus purpurascens*

132

133 SITE

134 111.1(29)

135 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

28 15
N₁ Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu
1 10 15

Cys Ser Lys Phe Cys Leu Xaa Gly Val Cys Phe Gly
25

10 - 136
11 - 79
12 - RTT
13 - 2 nus purpurascens

SITE
 (11-19)
 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residues 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lfinyl-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
 or hydroxy-Pro

406-146
Met Ala Lys Met Ala Met Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
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Asp Tyr Ser Met Phe Cys Leu Xaa Gly Val Cys Pro Gly
25

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2. 2. 2.	2. 2. 2.
3. 3. 3.	3. 3. 3.
4. 4. 4.	4. 4. 4.

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1 167
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Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
10 15

90
 TAA AAG CCG GTC ACG GCT GAT GAC TCC AGA TAT GGA TTA AAG AAT CTT
 Stop Thr Thr Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 30

144
 114 Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 40 45

192

aga aag aca gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt
Arg Lys Arg Asn Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
55 60

240
 gag ggg ttt tgc ttt tta tgg tcc ata aca ttt
 Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
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<401> 150
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asp Lys Arg Asn Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60

Ile Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

Val Asp Ser Gly

210 150
 211 30
 212 IFT
 213 *Onchus natus*

210 SITE
 211 SITE
 212 SITE
 213 Kaa at residue 4 may be Trp, 115-1-Tyr, mono-iodo-Tyr, di-iodo-Ty
 2, O-sulpho-Tyr or O-phospho-Tyr; Kaa at residue 14 may be Pro or
 hydroxy-Pro; Kaa at residue 20 may be Glu or gamma-carboxy-Glu;
 Kaa at residue 25 may be Trp or bromo-Trp

<401> 150
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 1 5 10 15

Cys Cys Ser Kaa Phe Cys Phe Leu Kaa Cys Ile Thr Phe Val Asp Ser
 20 25 30

210 150
 211 30
 212 IFT
 213 *Onchus natus*

210 SITE
 211 SITE
 212 SITE

210 160
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

210 160
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30

210 160
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 55 60

aca aia ctt tgc tgc aac ggg ata tgc tta tgg ttt gtc tgc ata tga 240
 Pro Tyr Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

ttt gat ttt ttaattgatgt cttctctctcc cctc 273
 Phe Asp Phe

4114 161
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 4112 PFT
 4113 *Chinus magus*

4114 161
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Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
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Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Asn Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
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Ile Gly Leu Lys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

166 Asp Phe

16 161
 111 81
 112 PFT
 113 *Chinus magus*

166 161
 111 321
 112 Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue
 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr; Xaa at residues 5, 6 and 14 may be Pro or hydro
 xy-Pro

166 161
 Arg Xaa Tyr Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Glu Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
 20 25 30

166 161
 111 81
 112 PFT
 113 *Chinus magus*

166 161
 111 81
 112 PFT
 113 *Chinus magus*

<100> 163
 arg aaa ctg acg tgc gtg atg atc gtt get gta ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Tyr Arg Thr Gln Asn Ser Lys Asp Leu
Tyr Met Phe Val Thr Ala Asp Ser Arg Tyr Gly Leu Lys Asp Leu

ttt cct aat gaa atg aag aac acg gaa ggc tct aaa ttg 144
Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
3' 4' 4'

540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450

ara gaa ctt tgc tgc aac gag ttt tgc att ctt tag tgc ata aca ttt 240
 ttc gcy leu cys cys ser glu phe cys tta leu tip cys ile thr phe
 66 70 75 80

glt gln thr ggc *aactjgig cgttggtga tctctctctc tccctac
*ac Asn Ser Gly

1.27	104
1.28	34
1.29	257
1.30	3 pure males

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 16 11

Tyr Trp Thr Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 25 30

Pro Phe Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
4) 35

Asn Glu Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
55 60

His Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
(8) 70 75 80

Val Asp Ser Gly

100 165
101 75
102 18T
103 *Scorus magus*

0011 - PITS
 0012 - 11. (37)
 0013 - Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residue 11 may be Pro or hydrox
 y-Pro; Xaa at residue 25 may be Tyr or bromo-Tyr

4499. 165
Xaa Ala Cys Xaa Asn Ala Gly Ser Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Ile Leu Xaa Cys Ile Thr Phe Val Asp Ser
20 25 30

<11> 166
<11> 171
<11> PNA
<11> Conus magus

<11>
<11> 108
<11> (111,1219)

<11> 108 48
acc aac cca acc tgc atg atg atc gtt gct gta ctg tta ttg acc gcc
Met Tyr Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Ile Thr Ala
1 5 10 15

tac aca ttc gtc acc gct gat gac tcc aga tat gca ctg aag gat ctg 96
Tyr Ile Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

tac tcc ttc gaa cgt cat gaa atg aag aac ccc gaa gcc ttt aaa ttg 144
Phe Thr Cys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

atc aca gaa gaa gcc tgc tat aat gct ggt aca ttt tct tgc atc aaa 192
Asp Thr Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
50 55 60

tta gaa ctt agc tgc agc gag ata ttc tca tca ttt gtc tgc ata tca 240
Ile Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

ttt gat ttg atgtatgtct tctctctccc tc 271
Ile Asp Leu

<11> 107
<11> 103
<11> PNT
<11> Conus magus

<11> 10
acc aac cca acc tgc atg atg atc gtt gct gta ctg tta ttg acc gcc
Met Tyr Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Ile Thr Ala
1 5 10 15

tac aca ttc gtc acc gct gat gac tcc aga tat gca ctg aag gat ctg
Tyr Ile Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

tac tcc ttc gaa cgt cat gaa atg aag aac ccc gaa gcc ttt aaa ttg
Phe Thr Cys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

atc aca gaa gaa gcc tgc tat aat gct ggt aca ttt tct tgc atc aaa
Asp Thr Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
50 55 60

tta gaa ctt agc tgc agc gag ata ttc tca tca ttt gtc tgc ata tca
Ile Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

Ile Asp Leu

<11> 108
<11> 103
<11> PNT
<11> Conus magus

Pro Tyr Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
6 75 75 80

Gly

410 101
411 35
412 PFT
413 *Canus semineus*

414

415 SITE

416 111..(12)

417 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or 6-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Phe or hydroxy-Phe

418 171
Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

419 Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

420 171
421 171
422 LNA
423 *Canus purpurascens*

424
425 PFT
426 111..(143)

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1000 171

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Ile Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

0.9

110- 171

111- 24

112- PBT

113- *Conus purpurascens*

114

115- SITE

116- 410...GP

117- Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 4 may be Tyr, 123-I-Tyr, methionine-Tyr, di-iodo-Tyr, O-su
pho-Tyr or S-phospho-Tyr; Xaa at residues 11 and 24 may be Pro or
gamma-carboxy-Pro

118- 114

119- Ala Cys Met Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
5 10 15

120- Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

110- 171

111- 24

112- PBT

113- *Conus striatus*

114

115- CPG

116- 410...240

118- 173

119- aa ctt agt tgg gtt atg att gtt gct gta cta ttg tgg acc act 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

120- aa cta ttc acc gct gat gac ttc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

121- aa aag tca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Ile Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

122- aa tga gaa ggg tgc tct aat ggt ggt aca ttt tat ggc atc cat 192
Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

123- aa gga ctc tgc tgc aac gag ttt tgg ttt ctt tgg ttc ata aca ttt 240

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
61 70 75 80

atg gat tgaatgcttc tctcccttc
116 Asp

266

116 178
117 81
118 957
119 Cetus striatus

116 178
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

Ile Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

116 Asp

116 178
117 81
118 957
119 Cetus striatus

116
117 SITE
118 (111,121)
119 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 11 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tr
p or homo-Trp

116 178
Met Gly Cys Ser Ser Gly Gly Thr Ile Cys Gly Ile His Xaa Gly Leu
1 5 10 15

116 Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

116 178
117 106
118 118A
119 Cetus striatus

116
117 CFS
118 (111,1246)

116 178
Met Lys Thr Ser tgc gtc atg atc gtc gct gtc ctc ttc acc act
1 5 10 15
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr

48

tga aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu

96

20 25 30
 ttr cca aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Phe Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aar aar aar gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
 Asn Lys Ala Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 cca aca cta tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 att gat tatgtattc tctctccctc 266
 Ile Asp
 110 170
 111 80
 112 PFT
 113 *Conus striatus*
 120 170
 Met tps leu Thr Cys Val Met Ile Val Ala Val Leu Phe leu Thr Thr 15
 1 5 10
 Ttr Ser Ile Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu 30
 11 15
 Phe ttr Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 45
 25 40 45
 Asp ttr Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His 60
 55 60
 Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe 80
 65 70 75 80
 Ttr Asp
 130 180
 131 70
 132 PFT
 133 *Conus striatus*
 140 180
 141 SITE
 142 (11...81)
 143 Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or br
 ome-Tip
 150 180
 Arg Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu 15
 5 10
 ttr ttr Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp 30
 15 25 30
 160 181
 161 81
 162 PFT
 163 *Conus striolatus*

12. SITE

12.1 (1) (21)

12.2 Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residue 11 may be Glu or gamma-carboxy-Glu

12.3 181

12.3.1 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.3.2 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

12.4 182

12.5 185

12.6 186

12.7 187

12.8 188

12.9 (1) (2147)

12.9.1 182
12.9.1.1 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.9.1.2 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

12.9.1.3 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.9.1.4 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

12.9.1.5 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.9.1.6 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

12.9.1.7 183

12.9.1.8 184

12.9.1.9 185

12.9.1.10 186

12.9.1.11 187

12.9.1.12 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.9.1.13 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

12.9.1.14 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

12.9.1.15 Cys Lys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
20 25 30

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
6 70 75

110 184
111 37
112 PPT
113 *Stenus catus*

114
115 SITE
116 (11...127)
117 Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
s, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

118 184
119 Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

120 Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
20 25

121 184
122 345
123 PPT
124 *Stenus catus*

125
126 184
127 (11...134)

128 184
129 atg atg atg atg atg atg gtt gct gta cta tta ttg acc gcc 48
130 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

131 thr aca atc atc aag ggt gat gac tcc aga tat gga ctg aag aat ctt 96
132 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

133 trt atg aag aga ggt cat gaa atg aag aac cgc gaa gcc tct aaa ttg 144
134 Ile Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

135 aac agg aga tat ggg tgc tct aat gat ggt gaa ttt tct ggc atc cat 192
136 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

137 tca gaa atc tgc tgc agc gag ctt tgc atg ggt tgg tgc aca 234
138 Met Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75

139 ttttgtcat tttactgtata caattttggg attcaacgga ggaacttgtct gcagcaacct 294

140 tttttttt ttgtgtgttt aatatttgtt gatgtctttt ctatttacct c 345

141 186
142 34
143 PPT
144 *Stenus catus*

145 186
146 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15
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 35 40 45
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60
 Leu Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
 65 70 75

100 187
 111 197
 113 197
 114 Citrus latens

115
 116 NITE
 117 (115-127)
 118 Met at residue 1 may be Tyr, 115-1-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr; Met at residue 14 may be Pro or
 hydroxy-Pro; Met at residue 26 may be Glu or gamma-carboxy-Glu;
 Met at residue 25 may be Trp or bromo-Trp

100 188
 Ala Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Met Gly Leu
 5 10 15

101 Cys Cys Ser Met Leu Cys Leu Gly Met Cys Thr
 20 25

116 189
 117 196
 118 DNA
 119 Some distans

119
 121 118
 122 (11...1246)

100 188
 Met Ala Cys Arg tgt ctg atg atc att gct atg cng ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

101 189
 Met Ala Cys Arg tgt ctg atg atc att gct atg cng ttc ttg acc gcc 96
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

102 190
 Met Ala Cys Arg tgt ctg atg atc att gct atg cng ttc ttg acc gcc 144
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

103 191
 Met Ala Cys Arg tgt ctg atg atc att gct atg cng ttc ttg acc gcc 192
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

104 192
 Met Ala Cys Arg tgt ctg atg atc att gct atg cng ttc ttg acc gcc 240
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15

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Phe Ser

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<113> *Conus distans*

<110> 185

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Phe Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

110 Ser

<110> 190
<111> 81
<112> PFT
<113> *Conus distans*

<110> 190
<111> 81
<112> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
Glu or gamma-carboxy-Glu

<110> 190
Phe Xaa Cys Xaa Leu Leu Val His Phe Cys Gly Ile Asn Gly Gly Leu
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Tyr Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

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<113> *Conus regius*

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<112> 111..(93)

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1 5 10 15 20 25 30
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tgatgtcttc tctctccatc

48

93

113

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 <111> *Conus regius*

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 e 7 may be Tyr, 125-I-Tyr, meta-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
 yr, or O-phospho-Tyr

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 118 Ile Tyr Gly Xaa Asp Xaa Met Phe Cys Gly Val Asn Val Phe Leu
 1 5 10 15
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Gln 75 Cys Ser 317 Trp Cys 117 Phe Ala Cys Leu
65 70 75

190
34
PAT
Genus gloriamaris

200- SITE
201 (18..201)
202 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
203 r, 6-sulpho-Tyr or 6-phospho-Tyr; Xaa at residue 18 may be Trp or
204 125-I-Trp

199
198 Nae Asx Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
5 10 15

Arg, Ser, Cys, Ile, Phe, Ala, Cys, Leu
20

110 100
111 100
112 100
113 100

11 12267

TCT GAG CTG ACG ATT ATC GTT GGT GTG CTA TTC TTG ACC GCC
Met Arg Leu Thr Val Ala Val Leu Phe Leu Thr Ala

18

...acc ttc gac acg gct ggg cct cac tcc agc aat gcg ttg gag aat
 100 Thr phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 45 70 95

144
 cat tat tgg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa
 leu tyr leu lys ala his his glu met asn asn pro glu asp ser glu
 40 45

192

114 aat agt agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac
115 aat agt tgc arg tgc tyr asp gly gly thr gly cys asp ser gly asn
56 55 60

5' ttt tgc agt agc tgc att ttc gtc tgc ctc taaaaactgcc 238
 6' cys cys ser gly trp cys ile phe val cys leu
 70 75

258

211 31
 212 36
 212 PPT
 213 Genus dalli

Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
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 5 40 45
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 50 55 60
 Gln Cys Tyr Ser Gly Trp Cys Ile Phe Val Cys Leu
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4110- 204
 4111- 70
 4112- PPT
 4113- *Onchus pennaceus*

4400- 204
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Phe Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn
 20 25 30
 Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
 35 40 45
 Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
 50 55 60
 Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
 65 70 75

4110- 205
 4111- 71
 4112- PPT
 4113- *Onchus pennaceus*

4200- SITE
 4201- (11...124)
 4202- Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
 4203- esidue 5 may be Trp or bromo-Trp; Xaa at residue 11 may be Pro o
 4204- r hydroxy-Pro

4400- 205
 Cys Phe Xaa Ser Xaa Val Ala Cys Xaa Ser Xaa Lys Arg Cys Cys Ser
 1 5 10 15
 His Val Cys Leu Phe Val Cys Thr
 20

4110- 206
 4111- 72
 4112- PMA
 4113- *Onchus distans*

4200- CDS
 4201- (11...126)

4400- 206
 Arg gaa ctg arg tgt atg ttg atc atc gct gtg ctg ttc ctg acg gcc 48
 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala 15
 1 5 10
 Ser gaa ctc tct aca aat gcg agt tac gcc aga agt aag cag aag cat 96
 Tyr Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His 30
 20 25
 Arg gtt ctg aag tgc act gac aaa aac tcc aag ttg acc cag cgt tgc 144
 Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys 45
 35 40
 Met gaa gct gaa gaa cat tgc act caa aat cct gac tgc tgc agt gag 192
 Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu

50 55 60
 tct ttc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 238
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 61 70 75
 tggatctcttccatc 253
 207
 76
 PPT
 Conus distans
 207
 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
 20 25 30
 Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
 35 40 45
 Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
 50 55 60
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 65 70 75
 208
 20
 PPT
 Conus distans
 208
 SITE
 11... (29)
 Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 11 may be Pro or hydroxy-Pro
 208
 Cys Asn Xaa Ala Gln Xaa His Cys Thr Gln Asn Xaa Asp Cys Cys Ser
 1 5 10 15
 Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 20 25
 209
 259
 DNA
 Conus ammiralis
 209
 YDS
 11... (226)
 209
 Arg aaG ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Ser Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gtg ccc gac ttc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
 20 25 30

ctt tat cag aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 3' 40 45
 ttg aac aag agg tgc tat gat ggt gga aca agt tct aac act gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
 55 60
 gaa tgc tgc agt ggc tgg tgc att ttc ctc tgc ctc taaaactgcc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
 65 70 75
 ctgatacttc cctcttcct c 259

1100- 210
 111- 70
 112- PFT
 113- *Conus ammiralis*

1400- 210
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
 50 55 60
 Cys Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
 65 70 75

1100- 111
 111- 14
 112- PFT
 113- *Conus ammiralis*

1200-
 121- SITE
 122- (11)-(24)
 123- Xaa at residue 2 may be Tyr, 125-1-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
 bromo-Trp

1400- 111
 Cys Xaa Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
 1 5 10 15
 Gly Xaa Cys Ile Phe Leu Cys Leu
 20

110- 112
 111- 180
 112- RNA
 113- *Conus textile*

120-
 121- PDS
 122- (24)-(155)
 1400- 112

ggcattacct aaaaatcac caag atg aaa ctg acg tgc atg atg atc gtt 51
Met Lys Leu Thr Cys Met Met Ile Val
1 5

ggt ggt ctg ttc ttg acc gcc tgg aca ttc gtc acc gct gcg cct cac 99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Ala Pro His
10 15 20 25

tgc ggt aat gcc tgg gag aat ctt tat ctg aag gca cat cat gaa atg 147
Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met
30 35 40

aac aac cgg gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg 195
Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly
45 50 55

aca agt tgt aac aat gga aac caa tgc tgc agt ggc tgg tgc att ttc 243
Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe
60 65 70

atc ttt tgc ctg taacctacc gtgagtttt ctctccgat c 286
Val Ser Cys Leu
75

1100 213

1110 27

1120 PPT

1130 Conus textile

1400 213

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Ile Val Thr Ala Ala Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu
65 70 75

1110 214

1120 25

1130 PPT

1140 Conus textile

1200

1210 SITE

1220 (1) 125

1230 Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp

1400 214

Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Val Ser Cys Leu
20 25

422- Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues 8 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be P or hydroxy-Pro

440- 217

Met Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser
1 5 10 15

Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly
20 25 30

Xaa

410- 218

411- 275

412- 1NA

413- Conus omaria

414- 219

415- 219

416- 219

417- 219

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Met Ser Lys Ser Arg Asp Glu Met Trp Asp Thr Asp Pro Ser Lys Leu
35 40 45

Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
50 55 60

Met Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
65 70 75 80

Met Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
85 90 95 100

418- 219

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440- 219

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Pro Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
35 40 45

Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
50 55 60

Ile Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

Cys Ala

110 113

111 11

112 11FT

113 Conus nalli

120 1

121 SITE

122 111..(31)

123 Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 15 may be Tyr, 1 16-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11, 12 and 16 may be Pro or Hydroxy-Pro

1400 113

Arg Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser
5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Lys Xaa Ser Phe Phe Cys Ala
20 25 30

110 124

111 171

112 124A

121 Conus nalli

130 1

131 124B

132 111..(252)

1400 124

141 aag atg aag tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

142 aen cta ctc atg gct gat tcc aac aat gga ctg gcg aat cat
Thr Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

143 tgn aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg
Pro Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

144 aea aag agg gat tgc aag gac gaa ttg gag ttt tgt ata gta cag gtc
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

145 att gga ttt gtg tat tgc tgc ccc tgg ctt atc tat ggc cct ttc gtc
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

ttg gtt tat atc tgaatgtcttc tateccctc
Cys Val Asp Ile

110 235
111 34
112 FET
113 Conus dalli

100 225
101 Cys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

102 Thr Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

103 Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

104 Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

105 Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

Cys Val Asp Ile

110 235
111 34
112 FET
113 Conus dalli

114 236
115 SITE
116 (1)..(33)
117 Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21
and 27 may be Pro or hydroxy-Pro;

118 236
119 SITE
120 (1)..(33)
121 Xaa at residue 16 may be Tyr, 135-I-Tyr, mono-iodo-Tyr, di-iodo-T
yr, O-sulpho-Tyr or O-phospho-Tyr

100 226
101 Cys Cln Gly Xaa Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe
5 10 15

102 Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp
20 25 30

103

110 237
111 65
112 DHA
113 Conus pennaceus

114 237
115 DMS
116 (1)..(234)

100 227
101 aaa ctg acg tgc ctg atg atc att gct gtg ctg ttc ttg acc gcc

SITE
(1)...(51)
Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue
7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr,
or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-
Pro

196- 19
197- Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
 5 10 15
198- Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30
199- 20
200- 21

0110 DNA
0111 Conus marmoreus

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0121 C18
0122 (132)...(209)

0123 280
atggacatc atccatcatcg atccatctgt ccacatcatct gtccatcatat ccattcattc 60
atctactgac aaactgtcat aaatatattga gtctctcttt ctgtttttat ctgacagatt 120
aaat gag aga jac tgc ctt aat gtt gat tat ttt tgc ggc ata cgg ttt 163
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
atc aac jac gag cha tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca 217
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
atc aac gag aag taactactgac gtgatgtctt ctctctccct ctagttagta 269
Phe Glu Gly Lys
35

0124 329
cagctgggag ctctagagga tccaaagetta cgtacggctg catcggaagt catagctctt 329
ctctagtgac aactaaattc aatttactgg cgtctcggtt tacaacgtgc tgactgggaa 349
0125 428
cactctggag ttaaccact taattgcctt gcagcacat

0130 241
0131 30
0132 FBI
0133 Conus marmoreus

0134 281
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
atc Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
Phe Glu Gly Lys
35

0140 242
0141 30
0142 FBI
0143 Conus marmoreus

0150
0151 SITE
0152 (11...30)
0153 Xaa at residue 6 may be Tyr, 125-L-Tyr, mono-iodo-Tyr, di-iodo-Tyr
or O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11 and 29 may be
Pro or hydroxy-Pro

0160 243
Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn Gly
1 5 10 15
Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Glu
20 25 30

110- 322
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 113- *Conus marmoreus*
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4100 036
4111 035
4112 DNA
4113 *Ocnus marmoreus*

4114
4115 M6
4116 (131)..(241)

4117 226
ggaaggccg ggaattcccg ggtgacatc atcatcatcg atcatctgt ccattccatcc 60
atccattat ccatttcgtg ccaaacctgtc ataacattt gactctctct ttctgttttt 120
atccacapa ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169
Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
1 5 10

ggt ata cag ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt 217
Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
15 20 25

ttt gtt tgc ata ggc aac aag tat taaaagccg ttagtcttc tattccatc 271
Phe Ile Tyr Ile Ala Glu Lys Tyr
30

tcattagtagt agggggccgc tctagaggat ccaagettac gtaagcgtgc atgcagcgtc 331
atccatttca tatagtgtca cctaaattca attcaattgc cgtcgtttta caagctcgtg 391
ctggcaaaa cccctggcgtt acccaactta atgcctttgc agcacatccc cctttcgcca 451
tctcagctaa tagccgaaga ggcccgcaac gatcgccctt ccccaacagtt gcgcagcctg 511
ccg ggcgaa gggg 525

4118 247
4119 37
4120 EST
4121 *Ocnus marmoreus*

4122 427
tcaasn glul arg asp cys leu glul pro asp tyr val cys gly ile pro 15
4 5 10
phe val phe asn gly leu cys cys ser gly ile cys val phe ile cys 30
20 25

ile ala glul lys tyr 35

4123 238
4124 33
4125 EST
4126 *Ocnus marmoreus*

4127
4128 SITE
4129 (1)..(33)
4130 Kaa at residue 4 may be Glu or gamma-carboxy-Glu; Kaa at residues
5 and 14 may be Pro or hydroxy-Pro; Kaa at residues 7 and 33 may
be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O

0113 - *Conus marmoreus*

0100 -

0101 - SITE

0102 - (1...21)

0103 - Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

0104 - 241

Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe

1

5

10

15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val

20

25

30

0105 - 241

0106 - 241

0107 - 241

0108 - *Conus maria*

0109 -

0110 - 241

0111 - (149)...(271)

0112 - 241

atagcggtt cggctgcagc tacgggtcgc gaattccggc gtgcacatca tcatcatcat 100

ctatcatcat gtccacccat caattcattc attcaatgac aaactgtcat aaatatttga 100

gattctttt ctgtttttat ctgcacaga ttg aac gag ada gac tgc ctt aat 172

Leu Asn Glu Arg Asp Cys Leu Asn

1

5

atg gat tat ttt tgt ggc ata cag ttt gtg aac aac agg ata tgc tgc 220

Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys

10

15

20

atg ggc aat tgt gtt ttt tct ctg cac acc cca agg gaa gta aaa ctg 268

Val Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu

30

35

40

atg gatgctcttc ccttcctctc tagtagtagt aggcgggcgc cctagaggat 321

Pro

ctaaatttcc gtacgctgtc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381

attacttgc cgtcgtttta caacgttgtg actgggaaaa ccttggcgtt acccaactta 441

atg ccttcttc agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgacgcg 501

atggccttcc ccaacagttg cgcagcctga atggggaatg ggacgcgcgc t 552

0113 - 243

0114 - 243

0115 - 243

0116 - *Conus maria*

0117 - 243

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro

1

5

10

15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu
20 25 30

His Thr Pro Arg Glu Val Lys Leu Pro
35 40

1210- 244
1211- 245
1212- PPT
1213- *Conus omaria*

1220- 246
1221- SITE
1222- (111)(37)
1223- Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 may be pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-carboxy-Glu

1230- 244
Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg
20 25 30

Xaa Val Lys Leu Xaa
35

1210- 245
1211- 246
1212- PPT
1213- *Conus obscurus*

1220- 246
1221- 247
1222- (180)...(181)

1230- 245
aaatgcacatg gacatccat ccattccatt attcattgag aaactgtaac aaatatccaa 60
gcctattctt cttgttttgt ctgac aga tgg aaa cgg tgc att gtt tac ggt 110
Arg Ser Lys Arg Cys Leu Val Tyr Gly
1 5

aaa cct tgt gac tgg ctg acc att gag ggt atg gag tgc tgc agt aaa 160
Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys
10 15 20 25

tgg tgc ttt atg atg tgc tgg taaaactgag gtaatgtttt ctactccct c 210
Lys Cys Phe Met Met Cys Trp
30

1210- 246
1211- 247
1212- PPT
1213- *Conus obscurus*

1240- 246
Arg Ser Cys Arg Cys Leu Val Tyr Gly Thr Pro Cys Asp Trp Leu Thr
1 5 10 15

Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp
20 25 30

118- 247
 119- 23
 120- 16T
 121- *Conus obscurus*

122- SITE
 123- (1)...(28)
 124- Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; Xaa at residue 17 may be Glu or gamma-carboxy-Glu

125- 247
 126- Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met
 1 5 10 15
 127- Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa
 20 25

128- 246
 129- 23
 130- 16A
 131- *Conus radiatus*

132- SITE
 133- 252
 134- (1)...(109)

135- 247
 136- aac bag aga gac tgc cat gaa gtt ggt gaa ttt tgt ggc tta cgg 49
 137- Asn Arg Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 1 5 10 15

138- ata aag aac ggg ata tgc tgc agt cag att tgt tta ggt gtc tgc 97
 139- Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30

140- aca atg ttt taaaaactgcc gtgatgtctt ctactccat 139
 141- Lys Val Phe
 35

142- 210
 143- 23
 144- 16T
 145- *Conus radiatus*

146- 243
 147- Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 5 10 15

148- Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30

149- Lys Val Phe
 35

150- 210
 151- 23
 152- 16T
 153- *Conus radiatus*

154- SITE

1000-1100
 1001-1100 Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 17 may be Pro or hydroxy-Pro

1000-1100
 1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15

1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15

1001-1100
 1001-1100
 1001-1100
 1001-1100 *Genus radiatus*

1001-1100
 1001-1100
 1001-1100 (100)

1001-1100
 1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15 49

1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15 97

1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15 133

1001-1100
 1001-1100
 1001-1100
 1001-1100 *Genus radiatus*

1001-1100
 1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15

1001-1100 Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
 5 10 15

1100

1100-1200
 1100-1200
 1100-1200
 1100-1200 *Genus radiatus*

1100-1200
 1100-1200
 1100-1200
 1100-1200
 1100-1200 Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
 residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr

1100-1200
 1100-1200 Xaa Val Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
 5 10 15

1100-1200 Xaa Val Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
 5 10 15

204 254
 205 143
 206 DNA
 207 *Conus radiatus*

208
 209 208
 210 100..(100)

211 204
 212 gat aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tog 49
 213 Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 214 5 10 15

215 ttt aag agc ttc cta tgc tgc act ggc ctg tgt gta ttc gtc tgc 97
 216 Ala Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 217 20 25 30

218 tggatgaact gccgtgatgt attctctctcc act 133
 219

220 205
 221 31
 222 PHT
 223 *Conus radiatus*

224 204
 225 Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 226 5 10 15

227 Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 228 20 25 30

229

230 250
 231 20
 232 PHT
 233 *Conus radiatus*

234
 235 SITE
 236 10..(29)
 237 Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu.

238 206
 239 Cys Thr Phe Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Ala Ser
 240 5 10 15

241 Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys Ile
 242 20 25

243 257
 244 103
 245 DNA
 246 *Conus radiatus*

247
 248 208
 249 100..(100)

250 217
 251 gat aag aga aaa tcc ttt ccc aaa aat cat ttt tgt ggc ttt gtg 49
 252 Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val

1 5 10 15 97
 ggg aag cgg aac tac cta tgc tgc agt ggc cgg tgt ata ttc gtc tgc
 Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30
 gtc ttttgaact ggggtgatgt cttctatccc cat 133
 Val
 1410 254
 1411 31
 1412 587
 1413 *Pinus radiatus*
 1414 218
 Met Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val
 1 5 10 15
 Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30
 Val
 1416 259
 1417 31
 1418 581
 1419 *Pinus radiatus*
 1420 219
 1421 NIFE
 1422 111..(28)
 1423 Xaa at residue 4 may be Pro or Hydroxy-Pro; Xaa at residue 17 may
 be Tyr, 115-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, C-sulpho-Tyr or O
 -sulpho-Tyr
 1424 229
 Cys Cys His Xaa Lys Asn His Phe Cys Gly Phe Val Val Met Leu Asn
 1 5 10 15
 His Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val
 20 25
 1426 260
 1427 130
 1428 GGA
 1429 *Pinus regius*
 1430 261
 1431 NIS
 1432 111..(29)
 1433 260
 Met Asp Arg Arg Arg tgc ctt cct cta gac tgg ttt tgt ggc ttc aat 48
 Val Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Val Cys
 1 5 10 15
 Met Asp Arg Arg ttt ctt tgc tgt agt ggc tac tgc ctt gtc gtc tgc 96
 Val Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
 10 15 30
 Met taaactgtc gtgatgtctt cttctccct c 130
 Met
 1439 261

6115- 30
 6116- 10T
 6117- *Cinus regius*

6118- 101
 101 Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
 1 5 10 15
 111- Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
 20 25 30

112-

6119- 161
 6120- 10
 6121- 10T
 6122- *Cinus regius*

6123-
 6124- 111E
 6125- 111..(10)
 6126- Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may
 be Trp or bromo-Trp; Xaa at residue 13 may be Tyr, 125-I-Tyr, meth
 i-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

6127- 10
 6128- Cys Leu Xaa Leu Asp Xaa Phe Cys Gly Phe Asn Ile Ile Gly Ala
 1 5 10 15

6129- Leu Cys Cys Ser Gly Xaa Cys Leu Val Val Cys Met
 20 25

6130- 103
 6131- 10
 6132- DNA
 6133- *Cinus Bolescertii*

6134-
 6135- 103
 6136- 10..(105)

6137- 103
 101 aa1 c1g aag tgt ctg ctg atc att gct gta ctg gtc ttg gca gcc 48
 102 Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala
 1 5 10 15
 111- cag ctg atc gta gct ggc gac tgc agt gat ggc cag gag aat cct 96
 112 Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Gln Asn Pro
 16 21 30
 121- c1g ag1 gca cct agc aat tcc tct ggg aag atg tca taa atg aag 144
 122 Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
 16 40 45
 131- t1g cag aca cgg ctg atg ttc ggc caa t1t tca tgg aaa aga cca 192
 132 Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
 16 51 60
 141- a1g ag1 ag1 tgc tgc atc ccc ggc ggc gaa aat tgt gat gta ttc cga 240
 142 Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
 16 70 75 80
 151- t1g cgg tgc tgc agt gga tat tgc ata cta ttc att tgc gca 285
 152 Tyr Arg Lys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala

85

90

95

319

tgataaagct gccttgatgt cttctctcc cctc

410 24

411 3

412 PFT

413 *Conus delessertii*

414 24

Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala
1 5 10 15

Cys Phe Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro
20 25 30

Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
35 40 45

Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
50 55 60

Ser Cys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
65 70 75 80

Leu Tyr Asp Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala
85 90 95

415 24

416 3

417 PFT

418 *Conus delessertii*

419 24

420 SITE

421 (1).....(28)

422 Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue
6 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 may
be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr

423 24

Arg Cys Ile Xaa Gly Gly Xaa Asn Cys Asp Val Phe Arg Xaa Xaa Arg
1 5 10 15

Cys Cys Ser Gly Xaa Cys Ile Leu Leu Cys Ala
20 25

424 24

425 1009

426 DNA

427 *Conus striatus*

428 24

429 CDS

430 (1).....(235)

431 24

432 misc feature

433 (1).....(1009)

434 S may be any nucleotide

435 24

gctggttgc ctcagggtac cggtcgggaa ttcccgggtc gacatcatca tcatgatgcc

60

atctgtccat ccatctatctt attcattcat tgcgtgccaa actgtattaa atattcaagt	170
ctctttttt gtttgtttct aacaga tta asa tgg ttc att cct agt ggt gaa	173
Leu Arg Trp Cys Ile Pro Ser Gly Glu	
1 5	
ctt ttt ttc cgc tcc gat ccc ata gaa tgc tgg agt ggc aag tgc gca	211
Leu Lys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala	
15 25	
tta gtc tgc ttg taaaactgcc gtgatgctt ctctcccat ctagttagtg	273
Pro Val Cys Leu	
tgcctggcgg ctctagagga tccangetta ctatagcgtg catgcgcagt catagctctt	332
ctcttttgtt acctaaattc aattacttg tcttgtttt acaacgttgt gattgggaaa	392
acgtgggtt taccnaattt aatcgcttg tgcacatctt ccttttgcgc agtggcgta	452
atagagaaga ggcgcgcacc gctgcctctt ctacacagtt tgcgcagctt gattggcgaa	512
tggaaagcg cctgtatggg cgcattaaac tggcgcggtt gtgggttggt taagccacag	572
tgtatagcta caattgcacg cgcctatagc tgcctgctct tctgtctctt ttccctctct	632
ttcttctctt gtttcggcg attttcccg taaagctctt aaatcggggt gcttcccttt	692
aaagtctctt gaattantgc tttaacggna ccttgaccc ccaaaaaaac ttggantaag	752
aggtatggg tctcttaant gggggtcacc tccctgaan agaaagcttt tctccctctt	812
tctctgtt ggtttctctt gtttttttaa aaagggacc tttttttccc aaaactggga	872
aaatctctaa acctatcttt tgggtctatt ttttgantt taaagggga ttttgcacca	932
tcttggtctt ttttggttga aaaaaaag cgggtttta aaaaaatttt accccaatt	992
ttaaaaaa tttttt	1052
213 167	
214 167	
215 167	
216 167	
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00110 173
 00111 18T
 00112 Genus obscurus

00113 176
 Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly Glu Val Cys Arg
 1 5 10 15
 Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys
 20 25 30

00114 177
 00115 18T
 00116 18T
 00117 Genus obscurus

00118 SITE
 00119 (117)(120)
 00120 Xaa at residue 3 may be Trp or bromo-Trp; Xaa at residue 6 may be
 Pro or hydroxy-Pro; Xaa at residues 9 and 15 may be Glu or gamma
 -carboxy-Glu; Xaa at residue 14 may be Tyr, 115-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

00121 187
 Val Arg Xaa Cys Val Xaa Ser Gly Xaa Val Cys Arg Arg Xaa Xaa Phe
 1 5 10 15
 Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser
 20 25

00122 172
 00123 184
 00124 18A
 00125 Genus radiatus

00126 173
 00127 183
 00128 (117)(122)...(117)

00129 173
 TTTCTCTCT CTTGCTGGG C AGG TGG ACT GGT TGC TGG CTT GAC GGA ACG 51
 Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr
 1 5 10

TTT TGC CTT TTT AGT AGG ATC AGA TGC TGC GGT ACT TGC AGT TCA ATC 99
 Val Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile
 15 20 25

TTA AAG TCA TGT GTG AGC TGATCGGGG GTTGATCTTC CTCCTCTGT 147
 Met Lys Ser Cys Val Ser
 30

TTCTATCTT TTTTGTGCTG AGTCTCTCTT ACGTGAGAGT GGTCTAGAAC CACTCATCAC 207

TTTCTCTCTT GGAGGCTTCA GAGGAGGTAC ATTGAAATAA AAGGTGCATT GC 259

00130 179
 00131 183
 00132 18T
 00133 Genus radiatus

44800 1273

Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
1 5 10 15

114 Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25 30

44800 1286

44811 18

44812 688

44813 *Corvus radiatus*

44800

44811 304E

44812 1111(28)

44813 Has at residue 3 may be Pro or hydroxy-Pro.

44800 3880

Cys Leu Asa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
5 10 15

114 Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

44800 441

44811 478

44812 604

44813 *Canus geographus*

44800

44811 570

44812 673(113)

44800 581

gaagattgga cagtgaaatt cagttcaatatt ttttttaattg tegtotttgg catcatccaa 60

aaatcatcaca ag atg aaa atg acg tgc atg atc atc gtt gct gtg atg ttc 111
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttg acc acc tgg aca ttc gtc acg gct gtg acc acc acc acc gat gta 159
Leu Phe Ala Tyr Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val
15 20 25

atg gag aat ctt tat atg aag gaa ctt acc gaa acg gaa acc acc gaa 207
Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu
30 35 40 45

acc acc aaa tgg aac atg aga gac gac gag tgc gaa cct cct gga gat 255
Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp
50 55 60

ttt tat agc ttt ttt aaa att ggg aag cct tgc tgc agt ggc tgg tgc 303
Leu Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Tyr Cys
65 70 75

tta acc tgg tgc gac taaaaactgac gtgatgtctt tttttccct atgtgtctacc 358
Phe Leu Phe Cys Ala
80

tggattacac ttgatgtggc gggtgcccct cagtggttat gaacccccct gagcagactc 418

tctgggggac tggggggttc aacatccaaa taaagcgaca acacaaatcac aagtaaaaaa 473

1210 180
 1211 82
 1212 PPT
 1213 Genus geographus

1214 180
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Asp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
 20 25 30
 Glu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

Cys Ala

1215 183
 1216 80
 1217 PPT
 1218 Genus geographus

1219 180
 1220 80...130
 1221 Xaa at residues 5 may be Glu or gamma-carboxy-Glu; Xaa at re
 1222 siduals 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues
 1223 24 and 28 may be Trp or bromo-Trp

1224 183
 Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
 1 5 10 15
 Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
 20 25 30

1225 144
 1226 118
 1227 DHA
 1228 Genus textile

1229 180
 1230 100
 1231 (2)...164

1232 180
 1233 misc_Feature
 1234 (1)...183
 1235 s. may be any nucleotide

1236 164
 30 ttc agg tgg act cta gag gag ttg gag aat ctt tat ctg aag gca 47
 Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala
 1 5 10 15
 caa cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc 95
 His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
 20 25 30

tat gat agt ggg aca agt tgt aac act gga aac caa tgc tgc agt ggc 143
Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly
 35 40 45

tgg tgc att ttc gtc tgc ctc taaaactgac gtgatgtctt ctactccct 194
 Tsp ¹⁹⁴ Phe Val Cys Leu
 191

cgctgtatgg taactgggtt gatctttgat tggcgagtgc ccttcactgg tlatgaaccc 254

crat atctcg actctctggg ggctctgggg atccaacatc aaaatanagg gacagcacia 314

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..10 - 245
..11 - 4
..12 - 3FI
..13 - Coccus textile

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1000 15
Lys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His
5 10 15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr
20 25 30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp
45 40 45

Arg Ile Phe Val Cys Leu

10 36
11 79
12 FBT
13 Corus textile

SITE
(1)-(14)
Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
Bromo-Trp

400 186
Gly Gaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
5 10 15

3.7 Naa Cys Ile Phe Val Cys Leu
29

210. 187
211. 480
212. 70A
213. *Cinus quercinus*

$$\begin{aligned} & \{1, 2, 3\} \\ & \{1, 2\} \quad \{1, 3\} \\ & \{1\} \quad \{2\} \quad \{3\} \quad \{1, 2\} \dots \{3, 3, 3\} \end{aligned}$$

400 207
jettlgtatt tctcgtgt ctctcttggc atcacccaaa acatcaccaa g atg aaa 57
Met Lys
1

ctg agc tgc atg atg atc gtt gct ctg ctg ttc ttg acc gcc tgg aca	105
Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr	
9 10 15	
ttc gac atg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga	153
Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly	
20 25 30	
tgg agc ctg gca gga gga tgg gag aaa ctt ttt cag atg gca cgc gac	201
Tyr Gly Glu Ala Gly Gly Tyr Trp Gly Lys Leu Phe Pro Met Ala Arg Asp	
35 40 45 50	
gaa atg aaa aac acc gaa gac tct aca ttg gac aat aag aga aag tgc	249
Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg Lys Cys	
55 60 65	
ggt gaa ggc ggt gaa gct tgc gta ata ctt atc att gga aac gta ttt	297
Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn Val Phe	
70 75 80	
ttc tgc aaa agc tcc tgt ctt ttc gtc tgc att agt taaactgctg	343
Cys Cys Lys Gly Tyr Cys Leu Phe Val Lys Ile Ser	
85 90	
ttgtgctt tactaacctc tgtgtacct ggcgtacct ttgattggcc tgtgcccttc	403
ttgtgttat agctgctgtg atcttacct ctggagacct ctgtggtcca acatccaaat	463
aaacaggcat cccaatg	480
1189 128	
1191 14	
1192 PRT	
1193 Conus quercinus	
1200 128	
Met Lys Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala	
1 5 10 15	
Trp Thr Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg	
20 25 30	
Gly Gly Trp Gly Glu Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala	
35 40 45	
Arg Asp Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg	
50 55 60	
Lys Cys Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn	
65 70 75 80	
Val Phe Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser	
85 90	
1199 129	
1201 14	
1202 PRT	
1203 Conus quercinus	
1210 SITE	
1211 (1)...(29)	
1212 Xaa at residue 6 may be Glu or gamma-carboxy-llu; Xaa at residue	
1213 11 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tyr, 125-1	

-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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1100 285
Cys Ala Ala Ala Gly Xaa Ala Cys Val Ile Xaa Ile Ile Gly Asn Val
      5          10          15

1110 Cys Cys Lys Gly Xaa Cys Leu Phe Val Cys Ile Ser
      20          25

1120 290
1121 410
1122 100A
1123 Conus leopardus

1130
1131 400S
1132 (1111246)

1140 295
atg aaa atg aag tgc tgc atc gtt gct gtg ctg ttc ttg acc gcc      48
Glu Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
      5          10          15

1150 ata ttc atc aag gct gat gac ttc aca aat gga ctg gag aat cgt      96
Thr Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
      20          25          30

1160 agg tag aca cgt gac aac atg aag aac gcc aaa gcc ttt aca tta      144
Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
      35          40          45

1170 gag aag aaa gag tgt gtt gaa ctt ggt gag att tgt gcc aca gcc      192
Ala Ile Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
      50          55          60

1180 atc tta gac gag gaa tgc tgc aat ggt tca tgc cat gtc ttc tgc      240
Arg Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
      65          70          75          80

1190 ata tagttaaact gctgtgatgt cttttttctt cctcgtgtgt acctggettg      296
Val Leu

1200
1201 ggttgttgt ggtgcctgtc cttcagtggt tgtgaaaccc ttgtacctta cttctctggac      356
1202 gcttttgtgt cccaacatcc aaataaaggc acatcctaatt gtaaaaaaaa aaaa      410

1210 301
1211 80
1212 157
1213 Conus leopardus

1220 291
Thr Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
      5          10          15

1230 tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta
      20          25          30          35          40          45          50          55          60          65          70          75          80          85          90          95

1240 tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta
      100          105          110          115          120          125          130          135          140          145          150          155          160          165          170          175          180          185          190          195

1250 tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta
      200          205          210          215          220          225          230          235          240          245          250          255          260          265          270          275          280          285          290          295

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Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
 65 70 75 80

Val Leu

110 121

111 121

112 121

113 121 *Canus leopardus*

114 121

115 121 SITE

116 121 121(30)

117 121 Xaa at residues 4, 7, 17 and 19 may be Glu or gamma-carboxy-Glu.

118 121

119 121 Xaa Cys Val Xaa Leu Gly Xaa Ile Cys Ala Thr Gly Phe Phe Leu Asp

120 121 5 10 15

121 121 Xaa Xaa Cys Cys Thr Gly Ser Cys His Val Phe Cys Val Leu

122 121 10 25 30

123 121

124 121

125 121

126 121 *Canus marmoreus*

127 121

128 121

129 121 121(231)

130 121

131 121 gaa gag aac tgc gtg gtg aac gtt gct gtg atg ttc ttg acc gcc 48

132 121 Phe Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala

133 121 5 10 15

134 121 gaa ttt gtc aac gct gat gac gcc aga aat gaa ttg gag aat ctt 96

135 121 Phe Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu

136 121 20 25 30

137 121 gag aag gaa ctt cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144

138 121 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu

139 121 35 40 45

140 121 gag aac tgc cct aac act ggt gaa tta tgt gat gtg gtt gaa gaa 192

141 121 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln

142 121 50 55 60

143 121 gag tgc tat aac tat tgc ttt att gta gtc tgc cta taaaactaac 241

144 121 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu

145 121 70 75

146 121 aaatgtctt ctactctcct ctgtgctgccc tggtctgctc ttgtattggc gctgtgacct 301

147 121 aaatgtctt gaaccccttg atccgacatc tgggg 336

148 121

149 121

150 121

151 121

152 121 *Canus marmoreus*

153 121

154 121

155 121 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60
 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75

0110- 295
 0111- 29
 0112- PPT
 0113- *Canis marmoreus*

0114- SITE
 0115- (1...126)
 0116- Xaa at residue 3 may be Pro or hydroxy-Pro; Xaa at residues 6 and 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or L-tyrosine-Tyr

0117- 298
 Phe Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 5 10 15
 Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
 20 25

0118- 296
 0119- 290
 0120- HHA
 0121- *Canis quercinus*

0122- CIS
 0123- (1...1340)

0124- 297
 atttcc atg aaa atg acg tat att gtc atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 tgg gcc tgg gct gat aac tcc aga aat gga ttc gag aat cga aat gga 96
 Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly
 15 20 25 30
 aaa cga aac aaa aac gaa atg aag aac atc gaa gcc tct aaa ttg aac 144
 Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn
 35 40 45
 tgc aga aac ggc gat tcc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg 192
 Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro
 50 55 60
 taa att gga ggg cca tuc tgt agt ggt tgg tgc ttt ttc gtc tgc tta 240
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Val Cys Leu
 65 70 75

110012gtg atgatgtctt ctaccacct ctgtgctacc tgaattgata ttgtattggc 300
 ctgtaccctt caatgggtat gaacacctct gatccgactc ttgtggaggcc tcgggggtcc 360
 attatgcava taatagcgaca gcaaaaaaaa aaaaaaaaaa aa 402

1101 297
 1101 298
 1101 299
 1101 300 *Conus guercinus*

1101 297
 1101 298 Thr Cys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 1101 299 Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg
 20 25 30
 1101 300 Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg
 35 40 45
 1101 301 Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile
 50 55 60
 1101 302 Gly Trp Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

1101 298
 1101 299
 1101 300
 1101 301 *Conus guercinus*

1101 302
 1101 303 SITE
 1101 304 (1)..< (20)
 1101 305 Xaa at residue 9 may be Glu or gamma-carboxy-Glu; Xaa at residues
 14 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp
 or bromo-Trp

1101 306
 1101 307 Asp Gly Asp Cys Val Asp Gly Gly Xaa Phe Cys Gly Phe Xaa Lys Ile
 1 5 10 15
 1101 308 Gly Gly Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
 20 25 30

1101 309
 1101 310
 1101 311
 1101 312 *Conus guercinus*

1101 313
 1101 314 PDS
 1101 315 (7)..< (215)

1101 316
 1101 317 misc feature
 1101 318 (1)..< (271)
 1101 319 n may be any nucleotide

1101 320
 1101 321 atg aat ctg acg tct gtc gtc atc gtt cct gtc cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc ggc ttg gct gat gac tcc aga aat gga ttg gag aat cga aat gaa 96
 thr ala leu ala asp asp ser arg asn gly leu glu asn arg asn glu
 1 20 25 30

caa gaa gta aac gaa aac gaa atg agg gac cgc cgg gac tgc caa gat 144
 gin glu arg asn glu met arg asp arg arg asp cys gin asp
 35 40 45

gag ggt gaa gtt tat ggc ttt ccg aaa cct gaa cca cac tac tgc agt 192
 ser gly val val cys gly phe pro lys pro glu pro his cys cys ser
 50 55 60

gag tgg tgc ctt ttc gtc tgc gcc taaaactggc gtgatgtcaa ataaagcgac 246
 gly trp cys leu phe val cys ala
 65 70

ccccatnna aaaaaaanaa aaaaaaa 274

110 300

111 70

112 PFT

113 Conus quercinus

300 300

gag lys leu thr cys val val ile val ala val leu phe leu thr ala
 1 5 10 15

leu ala asp asp ser arg asn gly leu glu asn arg asn glu gin glu
 20 25 30

asn asn glu asn glu met arg asp arg arg asp cys gin asp ser gly
 35 40 45

gag val cys gly phe pro lys pro glu pro his cys cys ser gly trp
 50 55 60

cys leu phe val cys ala
 65 70

110 361

111 24

112 PFT

113 Conus quercinus

300

111 SITE

112 312..(26)

113 Xaa at residues 12, 14 and 16 may be Pro or hydroxy-Pro; Xaa at r
 residue 15 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may b
 e Trp or bromo-Trp

300 301

asp cys gin asp ser gly val val cys gly phe xaa lys xaa xaa xaa
 1 5 10 15

gag cys cys ser gly xaa cys leu phe val cys ala
 20 25

110 362

111 340

112 IGA

113 Conus arenatus

320

6.12.1 (7) .. (246)

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0010 :
0011 : misc_feature
0012 : (17..(40)
0013 : n may be any nucleotide

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300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

acc acc tgg aca ttc gtc acg ggt gac tcc ata cgt gca ctg gag gat 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp
 10 20 25 30

ttt att ggg aag gga cgt gac gaa atg gaa aac aac gga gct tct coa 144
Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro
35 40 45

Lys Asn Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
50 55 60

Met Arg Gln Asp Ggg Gga Ggc Ggc Arg Gag Gtt Tgt Gca Att Atc Tgt 240
 Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
 70 75

gag tgg taacctct gatctactc ttggaagacc tccgggatcc aacatccaaa 296
Val Ser
26

f aaagaga tcccgatnaa aaaaaargaa aaaaaaaaaa asaa

340

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-10- 303
-11- 80
-12- EPT
-13- Cerus arenatus

```

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

Tig Trp Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
20 25 30

Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
35 40 45

Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
 50 55 60

His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
70 75 80

100 -04
11 -30
12 95T
130 Conus arenatus

SITE
(1), (30)

*203- Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 12S-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom-Trp

*400- 304

Asp-Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
20 25 30

*210- 305

*211- 381

*212- DNA

*213- *Conus arenatus*

*220-

*221- GUS

*222- (7)...(234)

*400- 305

ggaacc atg aaa ctg aag tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu
1 5 10

acc ggc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

aat gtt ttt cgg aag gca cgt ctc gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aga ttt aac cag agg tgc ctt gaa aag ggt gta gtt tgt gat ccg agt 192
Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
50 55 60

ggt cga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 134
Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

caaaactacc gtgatgtctt ctactccat ctgtgtctacc cctcgag 281

*10- 306

*211- 74

*212- PFT

*213- *Conus arenatus*

*400- 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly
50 55 60

Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

215- 307
211- 25
212- PFT
213- *Conus arenatus*

220-
221- SITE
222- (1)..< (25)
223- Xaa at residues 3 and 19 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro

230- 307
Cys Leu Xaa Lys Gly Val Leu Cys Asp Xaa Ser Ala Gly Asn Cys Cys
1 5 10 15
Ser Gly Xaa Cys Val Leu Val Cys Leu
20 25

210- 308
211- 287
212- PMA
213- *Conus arenatus*

214-
215- CDS
216- (27)..< (249)

2400- 308
2401- atg aaa ctg acg tgc atg gtg atc gtt act gtg ttg ttc ttg 48
Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu
1 5 10
2402- ggc tgg aca ttc tgc acg gct gat gac tcc aga aat gaa ttg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu
15 20 25 30
2403- ctc ttt ctg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa 144
Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys
35 40 45
2404- gar aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg 192
Glu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro
50 55 60
2405- att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc tgc tgc ttg 240
Gly Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75
2406- aaacctgac gtgatgtctt ctactcccat ctgtgctacc cctcgag 287

210- 309
211- 78
212- PFT
213- *Conus arenatus*

230- 309
Cys Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu Asn Leu
20 25 30
Ile Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp
35 40 45

1ys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro Lys Ile
60 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75

110 310

111 18

112 PPT

113 Conus arenatus

120

121 FITE

122 (1) (18)

123 Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residues
11 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tr
p or bromo-Trp

140 310

Xaa Cys Val Ala Gly Ser His Phe Cys Gly Phe Xaa Lys Ile Gly Gly
5 10 15

Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
20 25

110 311

111 400

112 ENA

113 Conus tessulatus

120

121 CDS

122 (7) (243)

140 311

Met Met atg aaa ctg acg tgt gtc gtc atc gtt gct gtc atg ttc ttg 49
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu
1 5 10

110 ggc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag 96
111 Ala Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

110 agc ggc ata tgg agg gaa cct ttg tcc aag gca cgt gac gaa atg 144
111 Arg Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met
35 40 45

110 ccc aac gtc tct aaa cgg gat tgc tgg cct aca tat tgg ttt tgt 192
111 Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys
50 55 60

110 ata cag agg gga tgc tgc cca agg act act tgc ttc ttc ctt tgc 240
111 Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys
65 70 75

110 tgggcatctc ttccactccc ttctgtgcta cctgggttga ccttgattg 293
111

110 tgggcatctc ttccactgggt ataaacccct ctgttccccc tctctggaag cttcgggggtg 353
111

110 tgggcatctc aaataaagg acgtccccc aaaaaaaa aaaaaaa 400
111

110 312

50 55 60
 att arg gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240
 Ile Phe Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile
 (6 70 75)
 taa tat gtc tagttgaact gcggtgatgt atttactacc cctctgtgct 289
 Tyr Cys Val
 (80)
 acgctgggtt tgatctttga ttgcccctgtg ccccttcaactg attatgaatt cctctgatcc 349
 Thr Arg Phe agacctcttg ggtccaaca tccaaataaa gcgacatccc aaaaaaaaaa 409
 ataaaaaa 419
 410- 315
 411- 81
 412- P51
 413- *Conus tessulatus*
 440- 315
 Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Ile Asn Ala
 1 5 10 15
 Thr Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu
 20 25 30
 Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu
 35 40 45
 Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile Ile Pro
 50 55 60
 Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile Tyr Cys
 65 70 75 80
 Val
 410- 316
 411- 29
 412- PPT
 413- *Conus tessulatus*
 420-
 421- SITE
 422- 111..(29)
 423- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 + Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydro
 xy-Pro; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, d
 i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 440- 316
 Met Lys Ala Leu Asp Gly Xaa Leu Cys Ile Ile Xaa Val Ile Gly Ser
 1 5 10 15
 Ile Ile Cys Cys His Gly Ile Cys Met Ile Xaa Cys Val
 20 25
 410- 317
 411- 408
 412- DNA
 413- *Conus imperialis*

4020-
4021- CDS
4022- (7)...(240)

400- 317
ggttcc atg aaa ctg acg tgc gtg gtg ttc gtt get gtg cag ttc ttg 48
Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu
1 5 10

atg gcc tgg gta ttc atc arg gct gat gac tcc aga aat gga atc gag 96
Thr Ala Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu
15 20 25 30

aat ttt cct cgg atg aga cgt cac gaa atg aag aac ccc aaa gcc tct 144
Asn Leu Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser
35 40 45

aat tgg aac aag aga cag tgc cgt gta gaa ggt gaa att tct ggc atg 192
Lys Leu Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met
50 55 60

ctg ttt gaa gca caa tgc tgc gat gg: tgg tgc ttt ttc gtc tgc atg 240
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
65 70 75

ttaaa-tggc gtgatgtctt ctactctcct cgtgtctacc tgcctgatac ttgattggc 300

tggagccctt cattggttat gaacccctct gatcctatcc tctggaggcc tcaggggctcc 360

agcatctaaa taaaggacaa tcacaatcaa aaaaaaaaaa aaaaaaaaaa 408

4030- 318
4031- 7:
4032- PPT
4033- Conus imperialis

400- 318
Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu Thr Ala
1 5 10 15

Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu Asn Leu
20 25 30

Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
35 40 45

Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met Leu Phe
50 55 60

Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
65 70 75

4040- 219
4041- 27
4042- PPT
4043- Conus imperialis

4050-
4051- SITE

4052- 711..(27)

4053- Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 5, 7 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 21 may be Trp or bromo-Trp

4400 312
Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln
1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met
20 25

4410 320

4411 321

4412 DNA

4413- Consensus characteristic

4420

4421 CDS

4422 (97)...(334)

4430 330

44300 atg aag ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

44300 ccc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96
Thr Ala Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
15 20 25 30

44300 att ttt tct cgg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

44300 aca tgc aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt cgg gga 192
Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
50 55 60

44300 ttt gga gat tgc tgc act ggc ttc tgc att tta gtc tgc atc 234
Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
65 70 75

44300 taaactcgcg gtgatgtctt ctactcccat ctgtgctaac cctcgag 281

4440 341

4441 342

4442 PFT

4443- Consensus characteristic

4450 351

44500 Ser Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

44500 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

44500 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

44500 Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
50 55 60

44500 Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
65 70 75

4460 362

4461 363

4462 PFT

4463- Consensus characteristic

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0000 SITE
0001 (1) .. (25)
0002 Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue
0003 6 may be Glu or gamma-carboxy-Glu

```

100 - 120
Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys
5 10 15

Thr Gly Phe Cys Leu Leu Val Cys Ile
25

110. 373
111. 377
112. DNA
113. *Cornus miliaris*

()..(240)

408- 379
 100% atg aaa ctg acg tgc gtg gtg atc gtt gct gta ttg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 5 10

400 ggc tgg aga ttc gtc atg gat gat gac tcc aga aat gat ttg gag 36
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
 20 25 30

atg att ttt ctg aag gca cgt cat gaa atg aag aac ccg gaa gct tct 140
Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser

35 40 45

aaa ttp aac aag aga tgc att cca aat ggt gta ctt tgt gat ctg gga
lys leu asn lys arg cys leu pro asn gly val leu cys asp leu gly

192

Met Cys Cys Thr Gln Gln Arg Gln Gln Gln Ala Ile Val Val Cys Ile 240
 Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
 65 70 75

287

010	324
011	78
012	FET
013	Conus miliaris

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
16 25 30

Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn. Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro
50 55 60

Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

65

70

75

1100 325
1110 17
1120 PPT
1130 Conus miliaris

1140
1150 SITE
1160 (1) (27)
1170 Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 12S-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp

1180 325
Met Leu Xaa Asn Gly Val Leu Cys Asp Leu Gly Ser Xaa Xaa Xaa Cys
1 5 10 15

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
20 25

1190 316
1200 343
1210 ENA
1220 Conus atlanticus

1230
1240 TDS
1250 (1) (240)

1260 316
1270 atg aaa ctg acg tgc gtg gtc atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

1280 ggc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

1290 tct ctt ttt cgg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser
35 40 45

1300 aat tgg aga ggg agg tgc cgt cct cgt ggt atg ttc tgt ggc ttt cgg 192
Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro
50 55 60

1310 aia cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc 240
Lys Pro Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
65 70 75

1320 taaaactggc gtgatgtgtt ctactcccat ctgtgctacc cctcgag 287

1330 327
1340 34
1350 PPT
1360 Conus atlanticus

1370 327
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu

23 25 30
 Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser Arg Ser
 35 40 45
 Asn Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro Lys Pro
 50 55 60
 Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
 65 70 75

110- 328
 111- 27
 112- PPT
 113- *Conus atlanticus*

114-
 115- SITE
 116- (1)...(27)
 117- Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at
 residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
 -sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bro
 mo-Trp

400- 313
 Cys Arg Xaa Arg Gly Met Phe Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
 5 10 15
 Cys Cys Asn Gly Xaa Cys Phe Ile Val Cys Ile
 20 25

110- 319
 111- 284
 112- IMA
 113- *Conus lividus*

114-
 115- C18
 116- (7)...(237)

1000- 329
 gatacc atc aaa ctg acg tgc gtg gtg atc gtt got gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
 15 20 25 30
 att gtt ttt tgg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 144
 Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
 aia tgc aac aag aag tgc cct aac act ggt gaa tta tgt gat gtg gtt 192
 Tyr Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
 50 55 60
 aia caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta 237
 Ala Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75
 aaactacc gtgagtgttt ctactccat ctgtgtacc cctcgag 284

100- 330

0110- 77
0111- PPT
0112- *Conus lividus*

0100- 381
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Phe Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 35 30
Ser Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60
Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

0110- 381
0111- 26
0112- PPT
0113- *Conus lividus*

0100- 381
0101- SITE
0102- (1)..< (26)
0103- Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may
be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr

0100- 381
Met Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15
Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
20 25

0110- 381
0111- 381
0112- 28A
0113- *Conus pulicarius*

0100-
0101- GDS
0102- (7)..< (234)

0100- 322
Met Met atg aaa atg acg tgc atg gtg atc gtt ggt gtg atg ttc ttg 48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
1 5 10
Met ggc tgg ata ttc gtc aag gct gat gac tcc aga aat gga ttg gag 96
Met Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu
15 20 25 30
Met ttt ttt cgg aag gca tgt cac gaa atg aag aac tcc aaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser
35 40 45
Met tta gac aag agt tgc gtt gaa gat ggt gat ttt tgt ggt cgg gga 192
Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly

50 55 60
 tat gaa gag tgc agt ggc ttc tgc ctt tac gtc tgc atc 234
 Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 ttaaaactcga gtpatgctt ctactcccat ctgtgtatcc cctcgag 281
 310- 313
 311- 36
 312- PPT
 313- *Genus pulicarius*
 340- 313
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 5 10 15
 Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Thr Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu
 50 55 60
 Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 310- 314
 311- 26
 312- PPT
 313- *Genus pulicarius*
 320-
 321- SITE
 322- (11)..< (25)
 323- Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and
 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr
 340- 334
 Lys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Cys Cys
 5 10 15
 Met Gly Phe Cys Leu Xaa Val Cys Ile
 20 25
 310- 336
 311- 386
 312- DHA
 313- *Genus generalis*
 320-
 321- GUG
 322- 371..< (349)
 340- 315
 gpatcc arg aaa ctg acg tgc gtg ggc atc gtt ggt gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc acg ggt gat gag acc aga tat aaa ctg gag 96

Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
15 20 25 30

aat cct ttt ctg aag gca ccc aac gaa ctg cag aaa cac gaa gcc tct 144
Asn His Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
35 40 45

gaa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg aag 192
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
50 55 60

cgg ttt ctt gaa gaa tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
65 70 75

gtt gaa acg taaaggcttg atgtcttcta ctccatctg tgcacacct agag 293
Ile Glu Thr
80

310 336
311 81
312 PFT
313 *Conus generalis*

400 336
Met Cys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro
20 25 30

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu
35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe
50 55 60

Arg Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu
65 70 75 80

Tha

310 337
311 82
312 PFT
313 *Conus generalis*

3000
301 SITE
302 (1)-(30)
303 Xaa at residues 9 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

400 337
Met Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala
5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr
20 25 30

310 358
311 400
312 DUA

113- *Conus episcopatus*

114- CDS

115- (7)... (134)

116- 338

atgcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 46
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc acc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
11 20 25 30

act att ttt tgg aat gta cat cac gaa atg aag aac ctc gaa gat tct 144
Asn Leu Ile Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser
35 40 45

aaa ttg aac aag aag tgc ctt ggg ttt ggt aaa gct tat ctt atg ctt 192
Gly Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu
50 55 60

att tca aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta 234
Thr Ser Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

taaaactaac gtagagcttt ctactcctct ctgtgctaac tggcttgatc ttgtattggc 294

gtgttgcttt cacttggttat gaacccctct gatcctactc tatgaagacc tctggggctcc 354

aaattcccaa taagagacaa tcacaaiaaa aaaaaaiaaa aiaaaa 400

117- 339

118- 76

119- PPT

120- *Conus episcopatus*

121- 338

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala 15
1 5 10

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu 30
20 25 30

Ile Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser Lys Leu 45
35 40 45

Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser 60
50 55 60

Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu 75
65 70 75

122- 140

123- 25

124- PPT

125- *Conus episcopatus*

126- 140

127- SITE

128- (1)... (25)

129- Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues 12 and 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s

ulpho-Tyr or G-phospho-Tyr

4470- 340
 Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
 1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu
 20 25

4480- 341
 4481- 404
 4482- DNA
 4483- *Corvus episcopus*

4490-
 4491- 022
 4492- (71) (740)

4490- 341
 4490- atg aaa ctg acg tgc gtg gtg atc att gct gtg atg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
 1 5 10

4491- ggc tag aba ttc gtc atg gct gat gac ccc aga gat gaa cgg gag 96
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu
 11 20 25 30

4492- gct gac gaa atg aac ccc gca ggc tct aaa ttg aac gag aga ggc 144
 Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly
 35 40 45

4493- ctt gca gtt gat tat ttt tgc ggc ata cgg ttt gtg agc aac ggg 192
 Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly
 50 55 60

4494- tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag 240
 Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

4495- taaactgac gtgacgtctt ctactccct cgtgctacc tggcttgatc ttgattgac 300

4496- gctgacatt cactgggtat gaacccctct gatcctactc tctgaagacc tctggggctc 360

4497- taaagcgcac taaagcgcac tcccaaaaa aaaaaaaaaa aaaa 404

4498- 342
 4499- 78
 4500- PET
 4501- *Corvus episcopus*

4500- 342
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys
 50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys

65

70

75

-110- 343

-111- 31

-112- PPT

-113- Genus episcopatus

-114-

-115- SITE

-116- (1)...(31)

-117- Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

-118- 342

Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn

1

5

10

15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln

20

25

30

-119- 344

-120- 340

-121- 30A

-122- Genus achatinus

-123-

-124- 318

-125- (85)...(171)

-126- 344

gaagactatg tccaccatct attattatct gctgcacaaac tctgtttaaatt attcaagtct 60

ttcttctcgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111

Leu Arg Trp Cys Ile Pro Arg Gly Asp

1

5

ttt tgt ttc ccc tgg gat cgc ata caa tgc tgc agt gcc aag tgc aca 159

Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr

10

15

20

25

tgc tgc tgc atg taaaactgcc gtgatgtctt ctactccct c 202

Phe Val Cys Met

-127- 345

-128- 34

-129- PPT

-130- Genus achatinus

-131- 345

Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg

1

5

10

15

Ile Ala Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met

20

25

-132- 346

-133- 34

-134- PPT

-135- Genus achatinus

-136-

-137- SITE

-138- (1)...(27)

112- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

1400- 346

Met Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

110- 347

111- 303

112- BHA

113- *Conus schatinus*

130

131- 313

132- (86)...(171)

1400- 347

gagagctctgg tctctctctct tctctctctc gctgccaac tgtattaaat attogaatct 60

ctctctctgt ttggtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111
Leu Arg Gly Cys Val Pro Ser Gly Glu
1 5

att ggt tag ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
15 20 25

tgc gtc tgc atg taaaactggc gtgatgtctt ctctctccat c 202
Ile Val Cys Met

110- 348

111- 39

112- PBT

113- *Conus schatinus*

1400- 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

110- 349

111- 27

112- PBT

113- *Conus schatinus*

130

131- SITE

132- (1)...(17)

133- Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1400- 349

Gly Cys Val Xaa Ser Gly Xaa Ile Cys Xaa Phe Met Asp His Ile Gly
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

010 350
011 261
012 CNA
013 *Conus bullatus*

020
021 C18
022 (1)...(234)

030 340
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 48
5 10 15

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 96
20 25 30

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 144
35 40 45

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 192
50 55 60

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 234
65 70 75

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 264

040 351
041 78
042 PFT
043 *Conus bullatus*

050 351
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 15
5 10

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 30
20 25

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 45
35 40 45

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 60
50 55 60

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala 75
65 70 75

060 352
061 17
062 PFT
063 *Conus bullatus*

070 SITE
071 (1)...(27)
072 Xaa at residues 2 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residues 6 and 14 may be Pro or hydroxy-Pro

-450- 352

Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu
 1 5 10 15

173 Cys Ser Xaa Phe Cys Phe Phe Ala Cys Phe
 20 25

-410- 353

-411- 276

-412- tRNA

-413- *Conus bullatus*

-420-

-421- CDS

-422- (11... (246)

-430- 353

atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga gac gct ccg gat agt gca 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
 20 25 30

aga aga tgg gag aaa ctt ttc tcc gag gaa cgt gac gaa atg aag aac 144
 Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
 35 40 45

acc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt 192
 Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
 50 55 60

acc atc ttt aaa aaa aac gat tgc tcc agt ggc ata tgc ata agc atc 240
 Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
 65 70 75 80

tgc ttg taaaactcgg tgatgtcttc tcttcccatc 276
 Cys Leu

-410- 354

-411- 87

-412- PPT

-413- *Conus bullatus*

-420- 354

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
 20 25 30

Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
 35 40 45

Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
 50 55 60

Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
 65 70 75 80

Cys Leu

-410- 355

111 27
112 PPT
113 Genus bullatus

120
121 SITE
122 (1) (27)
123 Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu

129 255
Gly Cys Leu Xaa Arg Xaa Xaa Phe Cys Xaa Ile Phe Lys Lys Asn Asp
1 5 10 15

Cys Cys Ser Gly Ile Cys Ile Ser Ile Cys Leu
20 25

10 356
11 268
12 CHA
13 Genus striolatus

136
137 253
138 (1) (237)

139 356
atg aaa atg agc tgc atg atg att ggt gct gtg atg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg ata ttt gca atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

act cag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Glu Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac cag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata 192
Asn Glu Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60

att gga aca atg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg 237
Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75

taaaactgac gtgatgtctt ctactccct 2 268

10 357
11 26
12 PPT
13 Genus striolatus

140 357
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Pro Glu Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75

110 - 358

111 - 35

112 - PPT

113 - Conus striolatus

120 -

121 - NITE

122 - (1)...(28)

123 - Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

400 - 354

Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
1 5 10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met
20 25

110 - 358

111 - 366

112 - DNA

113 - Conus consors

120 -

121 - CDS

122 - (1)...(246)

400 - 358

Atg gaa atg atg ttc atg atg atc gtt gct gtg atg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
5 10 15

atg aca ttc gtc atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Tyr Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccc aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tgc 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

aga gga ctc tgc tgc acc atc ctt tgc tta ttt ttc gtg tgc tta aca 240
Tyr Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

tct tgc tgaatgtcttc tctcccttc 266
Phe Ser

110 - 360

111 - 87

112 - PPT

113 - Conus consors

400 - 360

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

110 301

111 31

112 PPT

113 Cons. consors

114

115 SITE

116 (1)...(31)

117 Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
Glu or gamma-carboxy-Glu

118 361

Gaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

119 362

120 289

121 CMA

122 Cons. consors

123

124 CDS

125 (1)...(252)

126 363

127 aag atg acg tgc ctg atg atc gtt ggt gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

128 aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
1 20 25 30

129 ttc ccc aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
Ile Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
1 35 40 45

130 aag aga gat ggg tgc tat aat gct ggt aca ttt ttt ggc atc cgt 192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
1 50 55 60

131 gga ttc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
132 Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe

100 165
 gggccatct ggcacatcat ctattcattc attcgtctgc aaactgtatt aaatatccaa 60
 ggtctctctt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
 1 5 10

gat att tgt ttc ccc tgg gat cac ata caa tgc tgc aat gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
 15 20 25

gaa tgc ggc tgc ttg taaaactgcc gtgatgttt ctattccctc 205
 Ala Phe Val Cys Leu
 30

110- 366
 111- 31
 112- 187
 113- *Conus circumcisis*

1408- 366
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

110- 367
 111- 36
 112- PPT
 113- *Conus circumcisis*

120-
 121- SITE
 122- (1)..
 123- Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

1420- 367
 Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15
 Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25

110- 368
 111- 306
 112- 20A
 113- *Conus circumcisis*

120-
 121- CUS
 122- (13)..
 123- (175)

146- 368
 gnttcatttt gtccatccat ctattccattc attcgtgttc aaactgtatt aaatatccaa 60
 gttctctttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt agt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10

gat att tgt ttc ccc tgg gat cac ata caa tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
 15 20 25

gaa tgc tgc tgc ttg taaaactgcc gtgatgttt ctattccctc c 206
 Ala Phe Val Cys Leu
 30

110- 369
 111- 31
 112- PPT

0013- *Conus circumciscus*

0400- 363

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

0010- 370

0011- 37

0012- PKF

0013- *Conus circumciscus*

0020-

0021- SITE

0022- (1)...(27)

0023- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

0430- 370

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

Lys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

0010- 371

0011- 306

0012- DNA

0013- *Conus circumciscus*

0020-

0021- CDS

0022- (13)...(175)

400- 371
gatacactat gacacatcat ctattccattc attcgtctgc aaactgtatt aaatattcaa 60

gctctctctt cgttttggt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

ggt cct tgt ttc ccc tgg gat cac ata caa tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
15 20 25

aga ttc gtc tgc ttg taataactgcc gtgatgtctt ctctccct c 206
Ala Phe Val Cys Leu
30

0010- 372

0011- 31

0012- EPT

0013- *Conus circumciscus*

0400- 372

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

0010- 373

111- 36
112- PPT
113- Conus circumcissus

120-
121- SITE
122- (1)...(36)
123- Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

140- 373
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

150- 374
151- 396
152- SMA
153- Conus circumcissus

160-
161- 398
162- (83)...(175)

180- 374
gaatcatct gtcacatcat ctattcatct atttgtgccc aaactgtatt aaatattcaa 60

actatcttt ctgttttgtt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

act att tgt ttc ccc tgc gat cac ata xaa tgc tgc aat gcc gag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
15 20 25

gaa ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctccccc c 206
Ala Phe Val Cys Leu
30

190- 375
201- 31
202- PPT
203- Conus circumcissus

240- 375
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Ile Cys Phe Pro Ser
1 5 10 15
Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
20 25 30

250- 376
261- 26
262- PPT
263- Conus circumcissus

270-
271- SITE
272- (1)...(26)
273- Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residu
20 may be Glu or gamma-carboxy-Glu

280- 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
20 25

0110- 377
0111- 106
0112- DNA
0113- *Conus circumciscus*

0109-
0111- CDS
0112- (183)..(175)

400- 377
atgtccatct ggcacatccat ctatttcattc attcgtgtgc aaactgtatt aaatattcaa 60
tctctctt ctctttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tgg gat cac ata cga tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
15 20 25

gga ttc ttc tgc ttg taaaactgcc gtgatgtctt ctcttcccat c 206
Arg Phe Val Cys Leu
20

0110- 378
0111- 11
0112- PFT
0113- *Conus circumciscus*

0400- 378
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
5 10 15
Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

0110- 379
0111- 17
0112- PFT
0113- *Conus circumciscus*

0109-
0111- SI1E
0112- 41)..(27)
0113- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

0400- 379
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Arg
1 5 10 15
Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

0110- 380
0111- 106
0112- DNA
0113- *Conus circumciscus*

00200

0211 CDS

0222 (83)..(175)

0400 310

ggtacacatgt gtcacacatc ctatttcattc atttcgtgtgc aaactgtatt aaatatccaa 60

gttcctctctt ctgttttgtgt ct aac aga ttg act agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat att tgt ttc ccc tgg gat cac ata aac tgc tgc aat gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
15 20 25

gaa ttc gcc tgc ttg taaaaactgcc gtgatgtctt ctattccct c 206
Ala Phe Ala Cys Leu
30

0010 381

0211 31

0212 PPT

0213 Genus circumcisis

0400 381

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25 30

0010 382

0211 31

0212 PPT

0213 Genus circumcisis

0210

0211 SITE

0222 (1)..(26)

0223 Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

0400 382

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25

0010 383

0211 206

0212 CMA

0213 Genus circumcisis

0020

0221 CDS

0222 (83)..(175)

100 343

ggtacacatgt gtcacacatc ctatttcattc atttcgtgtgc aaactgtatt aaatatccaa 60

gttcctctctt ctgttttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tgg gat cac ata caa tgc tgc aat gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
 15 20 25

gaa ttc ptc tgc ttg taaaactgcc gtgatgtctt ctactccct c 206
 Ala Phe Val Cys Leu
 30

110- 384
 111- 31
 112- PPT
 113- *Conus circumciscus*

400- 384
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

110- 385
 111- 27
 112- PPT
 113- *Conus circumciscus*

110- SITE
 111- (1)..< (27)
 112- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
 1 may be Pro or hydroxy-Pro

400- 385
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
 1 5 10 15
 Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25

110- 386
 111- 290
 112- LNA
 113- *Conus circumciscus*

110-
 111- GDS
 112- (77)..< (169)

400- 386
 gttactctg tctctctcta ttattatctg ctgcacaaatg tattaatat tcaagtctct 60
 gttctgtgtt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
 1 5 10

gtt ttc ccc tgg gat cac ata caa tgc tgc agt gcc aag tgc aca ttc 160
 Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
 15 20 25

gac tgc atg taaaactgcc gtgatgtctt ctctctccct c 200
 Val Cys Met
 20

110- 387
 111- 31

0212- PPT
0213- *Conus circumciscus*

0214- 387
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser
1 5 10 15
Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25 30

0215- 388
0216- 37
0217- PPT
0218- *Conus circumciscus*

0219- SITE
0220- (11...127)
0221- Xaa at residue1 may be Trp or Bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

0222- 388
Xaa Cys Ile Xaa Thr Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15
Lys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

0223- 389
0224- 366
0225- CMA
0226- *Conus monachus*

0227-
0228- CTS
0229- (11...1246)

0230- 389
Arg Asn Arg Asn Trp Arg Atg Atc Gtt Gct Gtg Ctg Ttc Ttg Acc Gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Arg Asn Trp Gtc Asn Gct Gat Gac Tcc Aga Aat Gga Ttg Gag Aat Ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30
Ser Asn Arg Gln Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser 144
25 40 45
Asn Arg Asn Ser Gln Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn 192
50 55 60
Gln Gga Ctc Ttc Tgc Arg Asn Ctt Tgc Tta Ttt Ttc Gtg Tgc Tta Aca 240
65 70 75 80
Ctt Tcg Tgattgtttttt tttttttttt
Phe Ser 266

0231- 390
0232- 32
0233- PPT

02110- Genus monachus

02100- 390

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Met Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

02110- 391

02111- 31

02112- PPT

02113- Genus monachus

02110-

02111- SITE

02112- (1)...(41)

02113- Kaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Kaa at residue 2 may be Glu or gamma-carboxy-Glu

02100- 391

Kaa Kaa Cys Kaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

02110- 392

02111- 277

02112- DNA

02113- Genus stercusmuscarum

02120-

02121- CDS

02122- (1)...(146)

02100- 392

atc aac cag aag tgc atg atg atc att gct gtg atg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aca gct gat gac tgc ata aat aga cag gag aat aga 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
20 25 30

cac ara tgg gag aaa ctt ttg tgg aag gca cgt cac gaa atg aag aac 144
Arg Ile Trp Glu Lys Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
35 40 45

acc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
50 55 60

ttc cgc tgc gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240
 Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

tgc ttg taaaaactacc gtgatgtctt ctctctcccat c 277
 Cys Leu

110- 393
 111- 92
 112- PPT
 113- *Corvus stercusmuscarum*

1400- 293
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
 20 25 30

Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
 35 40 45

Phe Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
 50 55 60

Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

Cys Leu

110- 394
 111- 97
 112- PPT
 113- *Corvus stercusmuscarum*

120-
 121- SITE
 122- (1...127)
 123- Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
 Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
 -Glu

1400- 294
 Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Gln
 1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

110- 395
 111- 396
 112- CCA
 113- *Corvus stercusmuscarum*

120-
 121- CDS
 122- (1...1246)

1400- 295
 atg aaa ctg acg tgt gtg atg atc gtt gtt gtg ctg ttc ttg atc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 1 5 10 15

tgg aca ttc ttc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30
 ttt tgg aag gca cgt cat gaa atg aag aac ccc gaa ggc tct aaa ttg 144
 Ile Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 cca aga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 att gat tgaatgtcttc tattcccttc 266
 110 Asp
 110 396
 111 81
 112 PFT
 113 *Conus stercusmuscarum*
 400 396
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 110 Asp
 110 397
 111 81
 112 PFT
 113 *Conus stercusmuscarum*
 400 397
 Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Met Gly Leu
 5 10 15
 Cys Cys Ser Met Phe Cys Phe Leu Met Cys Ile Thr Phe Ile Asp
 20 25 30
 110 398
 111 105
 112 PDA
 113 *Conus striolatus*

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
20 25

4010 461

4011 47

4012 PDA

4013 Conus striolatus

4014

4015 CDS

4016 (127..(243)

4017 461

atg gaa cag acg tgc gtc atg atc gtt gct gtc ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala 15

agg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His 30

ttt tgg aag gaa cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu 15

gac aaa aag gaa gcc tgc tat cag act ggt act ttt tgt gcc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys 60

acc ggg ata tgc tgc agt gag ttc tgt tta cgc gcc gtc tgc gtc ggt 240
Thr Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly 80

agt taactgcact gatgtcttct attccctc 272
4017

4018 401

4019 81

4020 PFT

4021 Conus striolatus

4022 462

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala 15

Lys Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys 60

Pro Gly Leu Lys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly 80

4023

4024 463

4025 39

4026 PFT

4027 Conus striolatus

00200

0010 SITE

00200 (1)..(20)

00200 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

00300 403

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

0010 404

0011 265

0012 RNA

0013 Genus striolatus

00200

00200 405

00200 (1)..(146)

00300 404

atg aaa atg acg ggt ggt atg gct gtt gct gtg atg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

agg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

ggt acg aag gga agt ctc gaa atg aag aac ccc gaa ggc tct aaa tgg 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

atc aag aga tct gag tgc tat tct act ggt aca ttt ttt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

aga gga ttc tgc tgc agc aac ctt tgc tta ttt ttc gtc tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

ttt tgg tgatgtcttc tctccctc 265
Phe Ser

0010 405

0011 30

0012 PPT

0013 Genus striolatus

00300 405

Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn

10 55 60
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Val Cys Leu Thr
 65 70 75 80
 PHE Ser
 110 406
 111 31
 112 PPT
 113 Conus striolatus
 120
 121 SITE
 122 (1)..< (31)
 Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-icdo-Tyr, di-
 icdo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
 Glu or gamma-carboxy-Glu
 1400 406
 Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
 1 5 10 15
 Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
 20 25 30
 110 407
 111 227
 112 PMA
 113 Conus striolatus
 120
 121 PDS
 122 (1)..< (231)
 1400 407
 atg aaa atg aag tgt atg gtg atc gtc gcc gtg atg atc atg acc 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 agt cat atc atc acc ggt gat gac tcc aga ggt aag cag aag cat cgt 96
 Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 acc atg agg tgg act acc aaa gtc tcc aag tgg act agc tgc atg aaa 144
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45
 ggt ggg tct tat tgc gtc gct act aag aga atc tgc tgc ggt tat tgc 192
 Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
 50 55 60
 ggt tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatctctcc 241
 Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
 65 70 75
 aaatgtgc tctatcttt tctgctgat gtctctct cccctc 287
 110 408
 111 77
 112 ERT
 113 Conus striolatus
 1400 408

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
65 70 75

010 409

011 35

012 PPT

012 Conus striolatus

006

011 SITE

002 (1)..(35)

003 Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod
o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue
33 may be Pro or hydroxy-Pro

0400 409

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa
20 25 30

Xaa Lys Asn
35